

# SEQUENCE LISTING

<110> Bejanin, Stephane  
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

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<141> 2001-08-06

<150> US 60/305,456

<151> 2001-07-13

<150> US 60/302,277

<151> 2001-06-29

<150> US 60/298,698

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<151> 2001-05-25

<160> 112

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cgttgccaca	gttttgatga	tcattctctc	cccaaccaag	atggtggaaa	aagcaaaaac	180
gtggtgaatc	ttggagcaat	ccgacaaggc	atgaaacgct	tccaatttct	gttaaactgc	240
tgtgagccag	ggacaattcc	tgatgcctcc	atcctagcag	ctgccttgga	tctactatgc	300
ggcattcttc	tgattcattt	ttctccattt	gtgctgtttt	tctctgtgat	gtgaatccat	360
ccctatccat	tatgtcatgc	ctccatcttt	tgctgcttct	tcagattgca	ctgagccata	420
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ccgctgcaac	cgtggcaact	ggccagagtg	gatgaaaggg	caccacgtga	acatcaccaa	540
gaaaggactt	ccccggggac	gctctcccat	tgtgggcaac	aagcgaaacc	agaagctgca	600



Glu Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu  
85 90 95  
Asp Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu  
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Ile Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met  
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Lys Gln Lys Gly Lys Lys  
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Arg Ser Pro Val Pro Arg Trp Leu Leu Leu Leu Leu Gly  
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Leu Asn Ala Gly Ala Val Ile Asp Trp Pro Thr Glu Glu Gly Lys Glu  
1 5 10  
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Val Trp Asp Tyr Val Thr Val Arg Lys Asp Ala Tyr Met Phe Trp Trp  
15 20 25  
ctc tat tat gcc acc aac tcc tgc aag aac ttc tca gaa ctg ccc ctg 248  
Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu  
30 35 40 45  
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Val Met Trp Leu Gln Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly  
50 55 60  
aac ttt gag gaa att ggg ccc ctt gac agt gat ctc aaa cca cgg aaa 344  
Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys  
65 70 75  
acc acc tgg ctc cag gct gcc agt ctc cta ttt gtg gat aat ccc gtg 392  
Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val  
80 85 90  
ggc act ggg ttc agt tat gtg aat ggt agt ggt gcc tat gcc aag gac 440  
Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp  
95 100 105  
ctg gct atg gtg gct tca gac atg atg gtt ctc ctg aag acc ttc ttc 488





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&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; 1..19

&lt;400&gt; 6

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&lt;221&gt; 3'UTR

&lt;222&gt; 749..968

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&lt;221&gt; polyA\_site

&lt;222&gt; 953..968

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											-15				
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Leu	Gly	Leu	Leu	Met	Leu	Trp	Val	Ser	Gly	Ser	Ser	Gly	Asp	Ile	Val
		-10					-5					1			
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Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Val	Gln	Gly	Ser
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Asn	Tyr	Leu	Asp	Trp	Tyr	His	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Gln	Leu	
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Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg	Ala	Ser	Gly	Val	Pro	Asp	Arg	Phe	
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Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	
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Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Ala	Leu	Gln	Thr	
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Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr	Arg	Val	Asp	Ile	Lys	Arg	Thr	Val	
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gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	cag	ttg	aaa	484
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	
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Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	
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gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	aac	gcc	ctc	caa	tcg	ggt	aac	580
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	
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Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	
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Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	
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Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	
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Lys	Sér	Phe	Asn	Arg	Gly	Glu	Cys									
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Val	Thr	Pro	Gly	Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser
		15					20					25			
Leu	Leu	His	Val	Gln	Gly	Ser	Asn	Tyr	Leu	Asp	Trp	Tyr	His	Gln	Lys
	30					35				40					
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg	Ala
45					50					55				60	
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe
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          5                          10                  15  
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser  
          20                          25                  30  
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg  
35                          40                  45                  50  
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp  
                  55                  60                  65  
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser  
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gattaatcca tgggcaggcc tggaaaagt cccactccag tctgcgggac ccacagcctg 180  
gccctcaggc ctcaggcctt ccctggcttg aagattgggc ttcacctggg acctaccctt 240  
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289  
          Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala  
  -10  -5  
aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337  
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly  
          1                          5                          10                          15  
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385  
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys  
                  20                          25                          30  
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433  
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys  
                  35                          40                          45  
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481

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Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
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Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
      65                      70                      75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80                      85                      90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
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Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
      20                      25                      30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
      35                      40                      45                      50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
      55                      60                      65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
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Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
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gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcggggac ccacagcctg 180
gccctcaggc ctcaggcctt ccttggttg aagattgggc ttcacctggg acctaccctt 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
      Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
      -10                      -5
aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337

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Lys	Ala	Lys	Ser	Lys	Cys	Gly	Pro	Thr	Phe	Phe	Pro	Cys	Ala	Ser	Gly	
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Ile	His	Cys	Ile	Ile	Gly	Arg	Phe	Arg	Cys	Asn	Gly	Phe	Glu	Asp	Cys	
				20					25					30		
ccc	gat	ggc	agc	gat	gaa	gag	aac	tgc	aca	gca	aac	cct	ctg	ctt	tgc	433
Pro	Asp	Gly	Ser	Asp	Glu	Glu	Asn	Cys	Thr	Ala	Asn	Pro	Leu	Leu	Cys	
			35				40						45			
tcc	acc	gcc	cgc	tac	cac	tgc	aag	aac	ggc	ctc	tgt	att	gac	aag	agc	481
Ser	Thr	Ala	Arg	Tyr	His	Cys	Lys	Asn	Gly	Leu	Cys	Ile	Asp	Lys	Ser	
		50					55					60				
ttc	atc	tgc	gat	gga	cag	aat	aac	tgt	caa	gac	aac	agt	gat	gag	gaa	529
Phe	Ile	Cys	Asp	Gly	Gln	Asn	Asn	Cys	Gln	Asp	Asn	Ser	Asp	Glu	Glu	
	65				70						75					
agc	tgt	gaa	agt	tct	caa	gct	att	ttt	cca	caa	att	act	gtg	tcc		574
Ser	Cys	Glu	Ser	Ser	Gln	Ala	Ile	Phe	Pro	Gln	Ile	Thr	Val	Ser		
80					85				90							
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	5						10					15				
Ile	Gly	Arg	Phe	Arg	Cys	Asn	Gly	Phe	Glu	Asp	Cys	Pro	Asp	Gly	Ser	
	20				25						30					
Asp	Glu	Glu	Asn	Cys	Thr	Ala	Asn	Pro	Leu	Leu	Cys	Ser	Thr	Ala	Arg	
	35				40				45					50		
Tyr	His	Cys	Lys	Asn	Gly	Leu	Cys	Ile	Asp	Lys	Ser	Phe	Ile	Cys	Asp	
			55						60					65		
Gly	Gln	Asn	Asn	Cys	Gln	Asp	Asn	Ser	Asp	Glu	Glu	Ser	Cys	Glu	Ser	
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Ser	Gln	Ala	Ile	Phe	Pro	Gln	Ile	Thr	Val	Ser						
	85					90										

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gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcggggac ccacagcctg 180
gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccctt 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
      Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
            -10                      -5
aag gct aag tgc aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
      1              5              10              15
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
            20              25              30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
            35              40              45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
            50              55              60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
      65              70              75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80              85              90
tgagccctga gctaattaag tgctggataa gcacacctc ccagtaatcc tggtatcagc 634
ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggt 694
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Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
      20              25              30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
      35              40              45              50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
            55              60              65
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 Glu Glu Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys  
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 Val Leu Glu Ala Leu Glu Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro  
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 gtg tac tca gtc tat tca aag ctc cac cct cca gca cat tac cca cct 593  
 Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro  
 75 80 85  
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 Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly  
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 Gly Asn Tyr Met Gly Gln Ser Ile His Gln Val Thr Val Ala Gln Ser  
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 Tyr Ser Leu Gly Pro Asp Gln Ile Gly Pro Leu Arg Ser Leu Pro Pro  
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 Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu  
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Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr  
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135    140    145

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Tyr	Glu	Arg	Asp	Glu	Asp	Asn	Asn	Leu	Leu	Thr	Glu	Lys	Gln	Lys	Leu	
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<213> Homo sapiens

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	65	70
Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys		75
	80	85
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	100	105
Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp		110
	115	120
Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu		125
	130	135
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Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln		155
	160	165
Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala		170
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 Tyr Asp Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp  
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 Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr  
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 gtg ata ata ccc aat gag aaa agt ctt caa tta caa aaa gat gag gca 360



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Leu	Leu	Cys	Val	Cys	Leu	Ser	Gly	Ser	Val	Tyr	Cys	Glu	Glu	Val	Asp		
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cga	ttc	aac	aaa	att	aaa	aag	ctg	act	gcc	aaa	gat	ttt	gca	gac	ata	552	
Arg	Phe	Asn	Lys	Ile	Lys	Lys	Leu	Thr	Ala	Lys	Asp	Phe	Ala	Asp	Ile		
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Pro	Asn	Leu	Arg	Arg	Leu	Asp	Phe	Thr	Gly	Asn	Leu	Ile	Glu	Asp	Ile		
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Glu	Asp	Gly	Thr	Phe	Ser	Lys	Leu	Ser	Leu	Leu	Glu	Glu	Leu	Ser	Leu		
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Leu	Phe	Asn	Ala	Lys	Tyr	Asn	Lys	Ile	Lys	Ser	Arg	Gly	Ile	Lys	Ala		
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Cys	Lys	Ala	Asn	Asp	Thr	Ser	Tyr	Ile	Arg	Asp	Arg	Ile	Glu	Glu	Ile		
		240						245					250				
cgc	ctg	gag	ggc	aat	cca	atc	gtc	ctg	gga	aag	cat	cca	aac	agt	ttt	984	
Arg	Leu	Glu	Gly	Asn	Pro	Ile	Val	Leu	Gly	Lys	His	Pro	Asn	Ser	Phe		
		255					260				265						
att	tgc	tta	aaa	aga	tta	ccg	ata	ggg	tca	tac	ttt	taacctctat				1030	
Ile	Cys	Leu	Lys	Arg	Leu	Pro	Ile	Gly	Ser	Tyr	Phe						
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 Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile  
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 Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala Ile Thr  
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 Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys Leu Leu  
                   65                  70                  75  
 Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp Ile Asp  
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 Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala Arg Phe  
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 Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile Glu Asp  
                   130                  135                  140  
 Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu Ala Glu  
                   145                  150                  155  
 Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr Leu Phe  
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 Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala Asn Ala  
           175                  180                  185  
 Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His Asn Ala  
 190                  195                  200                  205  
 Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val Ile His  
                   210                  215                  220  
 Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe Cys Lys  
                   225                  230                  235  
 Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile Arg Leu  
           240                  245                  250  
 Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe Ile Cys  
           255                  260                  265  
 Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe  
 270                  275

<210> 23  
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 <212> DNA  
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<220>  
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 <222> 10..1212

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 <221> 3'UTR

<222> 1213..1746

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<221> polyA\_signal

<222> 1709..1714

<220>

<221> polyA\_site

<222> 1733..1746

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tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg	99
Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val	
1 5 10	
ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta	147
Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val	
15 20 25 30	
agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc	195
Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala	
35 40 45	
atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc	243
Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly	
50 55 60	
atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg	291
Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro	
65 70 75	
gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc	339
Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu	
80 85 90	
ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa	387
Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu	
95 100 105 110	
gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac	435
Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His	
115 120 125	
tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg	483
Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp	
130 135 140	
tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg	531
Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu	
145 150 155	
aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt	579
Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser	
160 165 170	
ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc	627
Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val	
175 180 185 190	
aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc	675
Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe	
195 200 205	
tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg	723
Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Pro Trp	
210 215 220	
aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac	771
Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn	
225 230 235	
cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg	819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val	
240 245 250	
gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca	867



[illegible]

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<211> 1239
<212> DNA
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<220>  
<221> 5'UTR  
<222> 1..126

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<220>
<221> CDS
<222> 127..879
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<221> 3'UTR  
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<220>
<221> polyA_site
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gccaggagag tcccgcacagg agtgtcaggt ttcaatctca gcaccagcca ctgagagcag 120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc 168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
              -20                      -15                      -10
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca 216

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Ser	Val	Cys	Ser	Met	Ser	Val	Leu	Arg	Ala	Tyr	Pro	Asn	Ala	Ser	Pro	
				-5					1				5			
ctg	ctc	ggc	tcc	agc	tgg	ggg	ggc	ctg	atc	cac	ctg	tac	aca	gcc	aca	264
Leu	Leu	Gly	Ser	Ser	Trp	Gly	Gly	Leu	Ile	His	Leu	Tyr	Thr	Ala	Thr	
		10				15						20				
gcc	agg	aac	agc	tac	cac	ctg	cag	atc	cac	aag	aat	ggc	cat	gtg	gat	312
Ala	Arg	Asn	Ser	Tyr	His	Leu	Gln	Ile	His	Lys	Asn	Gly	His	Val	Asp	
	25					30					35					
ggc	gca	ccc	cat	cag	acc	atc	tac	agt	gcc	ctg	atg	atc	aga	tca	gag	360
Gly	Ala	Pro	His	Gln	Thr	Ile	Tyr	Ser	Ala	Leu	Met	Ile	Arg	Ser	Glu	
40					45				50						55	
gat	gct	ggc	ttt	gtg	gtg	att	aca	ggg	gtg	atg	agc	aga	aga	tac	ctc	408
Asp	Ala	Gly	Phe	Val	Val	Ile	Thr	Gly	Val	Met	Ser	Arg	Arg	Tyr	Leu	
				60					65					70		
tgc	atg	gat	ttc	aga	ggc	aac	att	ttt	gga	tca	cac	tat	ttc	gac	ccg	456
Cys	Met	Asp	Phe	Arg	Gly	Asn	Ile	Phe	Gly	Ser	His	Tyr	Phe	Asp	Pro	
			75					80					85			
gag	aac	tgc	agg	ttc	caa	cac	cag	acg	ctg	gaa	aac	ggg	tac	gac	gtc	504
Glu	Asn	Cys	Arg	Phe	Gln	His	Gln	Thr	Leu	Glu	Asn	Gly	Tyr	Asp	Val	
	90						95					100				
tac	cac	tct	cct	cag	tat	cac	ttc	ctg	gtc	agt	ctg	ggc	cgg	gcg	aag	552
Tyr	His	Ser	Pro	Gln	Tyr	His	Phe	Leu	Val	Ser	Leu	Gly	Arg	Ala	Lys	
	105					110					115					
aga	gcc	ttc	ctg	cca	ggc	atg	aac	cca	ccc	ccg	tac	tcc	cag	ttc	ctg	600
Arg	Ala	Phe	Leu	Pro	Gly	Met	Asn	Pro	Pro	Pro	Tyr	Ser	Gln	Phe	Leu	
	120				125					130					135	
tcc	cgg	agg	aac	gag	atc	ccc	cta	att	cac	ttc	aac	acc	ccc	ata	cca	648
Ser	Arg	Arg	Asn	Glu	Ile	Pro	Leu	Ile	His	Phe	Asn	Thr	Pro	Ile	Pro	
				140					145					150		
cgg	cgg	cac	acc	cgg	agc	gcc	gag	gac	gac	tcg	gag	cgg	gac	ccc	ctg	696
Arg	Arg	His	Thr	Arg	Ser	Ala	Glu	Asp	Asp	Ser	Glu	Arg	Asp	Pro	Leu	
			155					160					165			
aac	gtg	ctg	aag	ccc	cgg	gcc	cgg	atg	acc	ccg	gcc	ccg	gcc	tcc	tgt	744
Asn	Val	Leu	Lys	Pro	Arg	Ala	Arg	Met	Thr	Pro	Ala	Pro	Ala	Ser	Cys	
	170						175					180				
tca	cag	gag	ctc	ccg	agc	gcc	gag	gac	aac	agc	ccg	atg	gcc	agt	gac	792
Ser	Gln	Glu	Leu	Pro	Ser	Ala	Glu	Asp	Asn	Ser	Pro	Met	Ala	Ser	Asp	
	185					190					195					
cca	tta	ggg	gtg	gtc	agg	ggc	ggg	cga	gtg	aac	acg	cac	gct	ggg	gga	840
Pro	Leu	Gly	Val	Val	Arg	Gly	Gly	Arg	Val	Asn	Thr	His	Ala	Gly	Gly	
	200				205				210					215		
acg	ggc	ccg	gaa	ggc	tgc	cgc	ccc	ttc	gcc	aag	ttc	atc	taggg	tcgct		889
Thr	Gly	Pro	Glu	Gly	Cys	Arg	Pro	Phe	Ala	Lys	Phe	Ile				
				220				225								
ggaagggcac	cctctttaac	ccatccctca	gcaaacgcag	ctcttcccaa	ggaccaggtc											949
ccttgacgtt	ccgaggatgg	gaaagggtgac	aggggcatgt	atggaatttg	ctgcttctct											1009
gggggtccctt	ccacaggagg	tcctgtgaga	accaaccttt	gaggcccaag	tcattgggggtt											1069
tcaccgcctt	cctcactcca	tatagaacac	ctttcccaat	aggaaacccc	aacaggtaaa											1129
ctagaaattt	ccccttcatg	aaggtagaga	gaagggggtct	ctcccaacat	atttctcttc											1189
cttgtgcctc	tcctctttat	cactttttaag	catgaaaaaa	aaaaaaaaaa												1239

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 <211> 251  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> 1..24

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Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu  
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 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg  
 10 15 20  
 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala  
 25 30 35 40  
 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala  
 45 50 55  
 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met  
 60 65 70  
 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn  
 75 80 85  
 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His  
 90 95 100  
 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala  
 105 110 115 120  
 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg  
 125 130 135  
 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg  
 140 145 150  
 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val  
 155 160 165  
 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln  
 170 175 180  
 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu  
 185 190 195 200  
 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly  
 205 210 215  
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile  
 220 225

<210> 27  
 <211> 1179  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..115

<220>  
 <221> CDS  
 <222> 116..961

<220>  
 <221> 3'UTR  
 <222> 962..1179

<220>  
 <221> polyA\_signal  
 <222> 1145..1150

<220>  
 <221> polyA\_site  
 <222> 1164..1179

<400> 27  
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 tgggtctctg actcattct gactttaggc gctcgaggac tgtgccagg agcag atg 118  
 Met  
 1  
 cgg ctc aga gcc cag gtg cgc ctg ctt gag acc cgg gtc aaa cag caa 166  
 Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln Gln

																214
																262
																310
																358
																406
																454
																502
																550
																598
																646
																694
																742
																790
																838
																886
																934
																981
																1041
																1101
																1161
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24



<221> UNSURE  
 <222> 116  
 <223> Xaa = Asn,Thr

<220>  
 <221> UNSURE  
 <222> 233  
 <223> Xaa = Phe,Ser

<400> 28  
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 Gln Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe  
 20 25 30  
 Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg  
 35 40 45  
 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser  
 50 55 60  
 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val  
 65 70 75 80  
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg  
 85 90 95  
 Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn  
 100 105 110  
 Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn  
 115 120 125  
 Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile  
 130 135 140  
 Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn  
 145 150 155 160  
 Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu  
 165 170 175  
 Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu  
 180 185 190  
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp  
 195 200 205  
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser  
 210 215 220  
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr  
 225 230 235 240  
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr  
 245 250 255  
 Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile  
 260 265 270  
 Arg Pro Asn Asp Phe Ile Pro Asn Val Ile  
 275 280

<210> 29  
 <211> 1118  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 1..344

<220>  
 <221> CDS  
 <222> 345..1118

<220>  
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 <222> 1103..1118

<400> 29

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tgtggcctgg gggaaggagg acgaggttct gcctggatcc cagcaggacg ctgtgccatt 120
tggaacaaa ggaatagtct gcctggaatc cctgcagatc ttggggccgg aggccagtcc 180
aacccttgga gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240
cgccccgcag tagctgcaga ctccgcccgc gacgtgtgcg cgcttctctg ggccagagcg 300
agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356
                                Met Gly Arg Thr

cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
-15                                -10                                -5                                1
tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
5                                10                                15
atc tgg gac gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500
Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val
20                                25                                30
gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
35                                40                                45
aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596
Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu
50                                55                                60                                65
gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644
Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser
70                                75                                80
gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692
Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys
85                                90                                95
gaa cag gca agt gca aag gca ggc aaa ggg gct agg gtg ggt acc atc 740
Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile
100                                105                                110
tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788
Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg
115                                120                                125
ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836
Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg
130                                135                                140                                145
gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884
Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala
150                                155                                160
cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat 932
Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr
165                                170                                175
aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980
Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn
180                                185                                190
atc ctg gag cga aca aat gat cct ttt att caa gaa gta gcc ttg gtc 1028
Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val
195                                200                                205
act ctg ggt aac aat gca gca tat tca ttt aac cag aat gcc ata cgt 1076
Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg
210                                215                                220                                225
gaa ttg ggt ggt gtc cca att att gca aaa aaa aaa aaa 1118
Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys Lys Lys
230                                235

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<210> 30

<211> 258

<212> PRT

<213> Homo sapiens

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<221> SIGNAL  
<222> 1..20

<220>  
<221> UNSURE  
<222> 49  
<223> Xaa = Glu, \*

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Gly Ala Gly Ala Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp  
1 5 10  
Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser  
15 20 25  
Xaa Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala  
30 35 40  
Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val  
45 50 55 60  
Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser  
65 70 75  
Gly Ser His Ser Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe  
80 85 90  
Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg  
95 100 105  
Val Gly Thr Ile Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys  
110 115 120  
Pro Gly Gly Arg Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg  
125 130 135 140  
Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys  
145 150 155  
Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe  
160 165 170  
Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln  
175 180 185  
Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu  
190 195 200  
Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln  
205 210 215 220  
Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys  
225 230 235  
Lys Lys

<210> 31  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> 1..13

<220>  
<221> CDS  
<222> 14..1048

<220>  
<221> 3'UTR  
<222> 1049..1273

<220>  
<221> polyA\_signal

<222> 1234..1239

<220>

<221> polyA\_site

<222> 1258..1273

<400> 31

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		-25				-20					-15					
tgc	ggc	cag	gcg	tgg	ggt	gcg	tcg	gtg	ggc	ggc	cgc	agc	tgc	gag	gag	97
Cys	Gly	Gln	Ala	Trp	Gly	Ala	Ser	Val	Gly	Gly	Arg	Ser	Cys	Glu	Glu	
		-10				-5							1			
ctc	act	gcg	gtc	cta	acc	ccg	ccg	cag	ctc	ctc	gga	cgc	agg	ttt	aac	145
Leu	Thr	Ala	Val	Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn	
	5					10					15					
ttc	ttt	att	caa	caa	aaa	tgc	gga	ttc	aga	aaa	gca	ccc	agg	aag	gtt	193
Phe	Phe	Ile	Gln	Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val	
20					25					30					35	
gaa	cct	cga	aga	tca	gac	cca	ggg	aca	agt	ggg	gaa	gca	tac	aag	aga	241
Glu	Pro	Arg	Arg	Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg	
				40					45					50		
agt	gct	ttg	att	cct	cct	gtg	gaa	gaa	aca	gtc	ttt	tat	cct	tct	ccc	289
Ser	Ala	Leu	Ile	Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	
			55					60					65			
tat	cct	ata	agg	agt	ctc	ata	aaa	cct	tta	ttt	ttt	act	gtt	ggg	ttt	337
Tyr	Pro	Ile	Arg	Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe	
		70				75						80				
aca	ggc	tgt	gca	ttt	gga	tca	gct	gct	att	tgg	caa	tat	gaa	tca	ctg	385
Thr	Gly	Cys	Ala	Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu	
	85					90					95					
aaa	tcc	agg	gtc	cag	agt	tat	ttt	gat	ggg	ata	aaa	gct	gat	tgg	ttg	433
Lys	Ser	Arg	Val	Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu	
100					105				110						115	
gat	agc	ata	aga	cca	caa	aaa	gaa	gga	gac	ttc	aga	aag	gag	att	aac	481
Asp	Ser	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn	
				120					125				130			
aag	tgg	tgg	aat	aac	cta	agt	gat	ggc	cag	cgg	act	gtg	aca	ggg	att	529
Lys	Trp	Trp	Asn	Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile	
			135					140				145				
ata	gct	gca	aat	gtc	ctt	gta	ttc	tgt	tta	tgg	aga	gta	cct	tct	ctg	577
Ile	Ala	Ala	Asn	Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu	
		150					155					160				
cag	cgg	aca	atg	atc	aga	tat	ttc	aca	tcg	aat	cca	gcc	tca	aag	gtc	625
Gln	Arg	Thr	Met	Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val	
		165				170				175						
ctt	tgt	tct	cca	atg	ttg	ctg	tca	aca	ttc	agt	cat	ttc	tcc	tta	ttt	673
Leu	Cys	Ser	Pro	Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe	
180					185					190					195	
cac	atg	gca	gca	aat	atg	tat	gtt	ttg	tgg	agc	ttc	tct	tcc	agc	ata	721
His	Met	Ala	Ala	Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile	
				200					205					210		
gtg	aac	att	ctg	ggt	caa	gag	cag	ttc	atg	gca	gtg	tac	cta	tct	gca	769
Val	Asn	Ile	Leu	Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala	
			215					220					225			
ggt	gtt	att	tcc	aat	ttt	gtc	agt	tac	gtg	ggg	aaa	gtt	gcc	aca	gga	817
Gly	Val	Ile	Ser	Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly	
		230					235					240				
aga	tat	gga	cca	tca	ctt	ggt	gca	gcc	ctg	aaa	gcc	att	atc	gcc	atg	865
Arg	Tyr	Gly	Pro	Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met	
		245				250					255					
gat	aca	gca	gga	atg	atc	ctg	gga	tgg	aaa	ttt	ttt	gat	cat	gcg	gca	913
Asp	Thr	Ala	Gly	Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala	

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260          265          270          275
cat ctt ggg gga gct ctt ttt gga ata tgg tat gtt act tac ggt cat 961
His Leu Gly Gly Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His
          280          285          290
gaa ctg att tgg aag aac agg gag ccg cta gtg aaa atc tgg cat gaa 1009
Glu Leu Ile Trp Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu
          295          300          305
ata agg act aat ggc ccc aaa aaa gga ggt ggc tct aag taaaactggg 1058
Ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Gly Ser Lys
          310          315          320
attggacagt agtgggtgcat ctgggtccttg ccgcctgaga gcccaggag acatcgggcta 1118
gagtgaccat ggctatgctc ccgtctggaa gatgccagca tctggcctcc cacttttttc 1178
agctgtgtcc cccagtcctg gtcttttttag aatgtgaatg atgataaagt tgtgaaataa 1238
aggtttctat ctagtttgca aaaaaaaaaa aaaaa 1273

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<210> 32  
 <211> 345  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..26

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<400> 32
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  -25          -20          -15
Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val
  -10          -5          1          5
Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
          10          15          20
Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
          25          30          35
Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
          40          45          50
Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
          55          60          65          70
Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
          75          80          85
Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
          90          95          100
Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
          105          110          115
Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
          120          125          130
Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
          135          140          145          150
Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
          155          160          165
Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
          170          175          180
Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
          185          190          195
Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
          200          205          210
Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
          215          220          225          230
Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
          235          240          245
Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
          250          255          260
Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
          265          270          275

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Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp  
 280 285 290  
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn  
 295 300 305 310  
 Gly Pro Lys Lys Gly Gly Ser Lys  
 315

<210> 33  
 <211> 723  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..72

<220>  
 <221> CDS  
 <222> 73..672

<220>  
 <221> 3'UTR  
 <222> 673..723

<220>  
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 <222> 689..694

<220>  
 <221> polyA\_site  
 <222> 708..723

<400> 33  
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 accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta 111  
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val  
 1 5 10  
 ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159  
 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser  
 15 20 25  
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207  
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg  
 30 35 40 45  
 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255  
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr  
 50 55 60  
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303  
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro  
 65 70 75  
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351  
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val  
 80 85 90  
 ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399  
 Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr  
 95 100 105  
 aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447  
 Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala  
 110 115 120 125  
 ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495  
 Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu  
 130 135 140  
 gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543  
 Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys



<221> polyA\_signal  
<222> 809..814

<220>  
<221> polyA\_site  
<222> 830..845

<400> 35  
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taaattctgc caaaaggact gaggaacggt gcctggaaaaa gggcaagaat atcacggc 118  
atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166  
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe  
1 5 10 15  
aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214  
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile  
20 25 30  
tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262  
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro  
35 40 45  
tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310  
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met  
50 55 60  
gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358  
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys  
65 70 75 80  
ctg ctt atg tgc ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406  
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu  
85 90 95  
gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454  
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser  
100 105 110  
atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502  
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser  
115 120 125  
atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550  
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp  
130 135 140  
acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598  
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly  
145 150 155 160  
tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646  
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg  
165 170 175  
ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695  
Gly Pro Tyr  
atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggt 755  
attatctctc tatcagataa gattttgtta atgtactatt ttactcttca ataaataaaa 815  
cagtttatta tcgcaaaaaa aaaaaaaaaa 845

<210> 36  
<211> 179  
<212> PRT  
<213> Homo sapiens

<400> 36  
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe  
1 5 10 15  
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile  
20 25 30  
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro  
35 40 45  
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met  
50 55 60



Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys  
65 70 75 80  
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu  
85 90 95  
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser  
100 105 110  
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser  
115 120 125  
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp  
130 135 140  
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly  
145 150 155 160  
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg  
165 170 175  
Gly Pro Tyr

<210> 37  
<211> 517  
<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> 1..16

<220>  
<221> CDS  
<222> 17..259

<220>  
<221> 3'UTR  
<222> 260..517

<400> 37  
ttccatagaa tgggag atg tca cca ggg cag cct atg aca ttc ccc cca gag 52  
Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu  
1 5 10  
gcc ctg tgg gtg acc gtg ggg ctg tct gtc tgt ctc att gca ctg ctg 100  
Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu  
15 20 25  
gtg gcc ctg gct ttc gtg tgc tgg aga aag atc aaa cag agc tgt gag 148  
Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu  
30 35 40  
gag gag aat gca gga gct gag gac cag gat ggg gag gga gaa ggc tcc 196  
Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser  
45 50 55 60  
aag aca gcc ctg cag cct ctg aaa cac tct gac agc aaa gaa gat gat 244  
Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp  
65 70 75  
gga caa gaa ata gcc tgaccatgag gaccagggag ctgctacccc tccctacagc 299  
Gly Gln Glu Ile Ala  
80  
tcctaccctc tggctgcaat ggggctgcac tgtgagccct gcccccaaca gatgcaccc 359  
gctctgacag gtgggctcct tctccaaagg atgcgataca cagaccactg tgcagcctta 419  
tttctccaat ggacatgatt cccaagtcac cctgctgcct tttttcttat agacacaatg 479  
aacagaccac ccacaacctt agttctctaa gtcaccc 517

<210> 38  
<211> 81  
<212> PRT  
<213> Homo sapiens

<400> 38



gga Gly	agg Arg	act Thr	gcc Ala	aac Asn	ctc Leu	tac Tyr	tcc Ser	ctt Leu	cac His	agc Ser	tgg Trp	ctg Leu	ggc Gly	atc Ile	acc Thr	628	
9095100																	
act Thr	gtc Val	ttc Phe	ctc Leu	ttc Phe	ggc Gly	tgc Cys	cag Gln	tgg Trp	ttc Phe	ctg Leu	ggc Gly	ttt Phe	gct Ala	gtc Val	ttc Phe	676	
105110115120																	
ctc Leu	ctg Leu	ccc Pro	tgg Trp	gcg Ala	tcc Ser	atg Met	tgg Trp	ctg Leu	cgc Arg	agc Ser	ctc Leu	cta Leu	aaa Lys	cct Pro	atc Ile	724	
125130135																	
cac His	gtc Val	ttt Phe	ttt Phe	gga Gly	gcc Ala	gcc Ala	atc Ile	ctc Leu	tct Ser	ctg Leu	tcc Ser	atc Ile	gca Ala	tcc Ser	gtc Val	772	
140145150																	
att Ile	tcg Ser	ggc Gly	att Ile	aat Asn	gag Glu	aag Lys	ctt Leu	ttc Phe	ttc Phe	agt Ser	ttg Leu	aaa Lys	aac Asn	acc Thr	acc Thr	820	
155160165																	
agg Arg	cca Pro	tac Tyr	cac His	agc Ser	ctg Leu	ccc Pro	agt Ser	gag Glu	gcg Ala	gtc Val	ttt Phe	gcc Ala	aac Asn	agc Ser	acc Thr	868	
170175180																	
ggg Gly	atg Met	ctg Leu	gtg Val	gtg Val	gcc Ala	ttt Phe	ggg Gly	ctg Leu	ctg Leu	gtg Val	ctc Leu	tac Tyr	atc Ile	ctt Leu	ctg Leu	916	
185190195200																	
gct Ala	tca Ser	tct Ser	tgg Trp	aag Lys	cgc Arg	cca Pro	gag Glu	ccg Pro	ggg Gly	atc Ile	ctg Leu	acc Thr	gac Asp	aga Arg	cag Gln	964	
205210215																	
ctg Leu	ctg Leu	cta Leu	cag Gln	ctg Leu	agg Arg	cct Pro	gga Gly	tcc Ser	cgg Arg	cct Pro	ttc Phe	cct Pro	gtg Val	act Thr	tac Tyr	1012	
220225230																	
gtg Val	tct Ser	gtc Val	acc Thr	ggc Gly	agg Arg	cag Gln	ccc Pro	tac Tyr	aaa Lys	tcc Ser	tgg Trp	tgacctgctc				1058	
235240																	
tcccaagaac			agagcctgtc			cccagatgtc			ccagtagcga			tgagtaacag			aggtggctgt		1118
ggacttccct			tactttctct			tgctggatca			gggccttcct			gcctcccgc			gggcaggtct		1178
ggccttgctc			tctttggcag			gccccagccc			ctctgaccac			tctgcagctc			accatgcagc		1238
tगतgcaaaa			gttgtgggtgt			ccagtgtgca			gcagccctgg			gagccactgc			caccttcaga		1298
ggggttcctt			ctctgagacc			acattgtcttc			acctggcccc			accatggctg			cttgccctggc		1358
ccaacctagc			gtttctgtgcc			atgctagaac			ttgagctgtt			gctcttcttc			aggggaggaa		1418
atagggtgga			gagcggggaag			ggtcttgctc			ctaagtgttg			ctgctgtggc			ttttttgcct		1478
tctccaaaga			cgcactgcca			ggtcccaagc			ttcagactgc			tgtgcttagt			aagcaagtga		1538
gaagcctggg			gtttgagacc			cacctactct			ctggcagcat			cagcatccta			ctcctggcaa		1598
catcaggcca			acgtccaccc			cagcctcaca			ttgccagatg								

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<210> 40
<211> 263
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> 1..20
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<400>	40														
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-20					-15					-10					-5
Gly	Ser	Met	Cys	Ile	Leu	Phe	Thr	Ile	Tyr	Trp	Met	Gln	Tyr	Trp	Arg
				1				5					10		
Gly	Gly	Phe	Ala	Trp	Asn	Gly	Ser	Ile	Tyr	Met	Phe	Asn	Trp	His	Pro
		15					20					25			
Val	Leu	Met	Val	Ala	Gly	Met	Val	Val	Phe	Tyr	Gly	Gly	Ala	Ser	Leu
	30					35					40				
Val	Tyr	Arg	Leu	Pro	Gln	Ser	Trp	Val	Gly	Pro	Lys	Leu	Pro	Trp	Lys



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Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala
      15      20      25
gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306
Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu
      30      35      40
ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354
Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro
      45      50      55
cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402
Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro
      60      65      70      75
ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450
Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val
      80      85      90
act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502
Thr Pro Asn Phe
      95
agtttctgcc tggccctgca tctgggtcca gccacactgc cctcccccttt ttcggggactc 562
tgtattccct cttgggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622
tcagcaaaaa aaaaaaaaaa a 643

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<210> 42  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..30

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<400> 42
Met Pro Ala Cys Arg Leu Gly Pro Leu Ala Ala Ala Leu Leu Leu Ser
-30      -25      -20      -15
Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys
      -10      -5      1
Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu
      5      10      15
Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala
      20      25      30
Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys
      35      40      45      50
Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln
      55      60      65
Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn
      70      75      80
Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe
      85      90

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<210> 43  
 <211> 501  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..227

<220>  
 <221> CDS  
 <222> 228..501

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<400> 43
actcttactc tttctctctc actctctctc ttttcccacc cttaagccaa gtacagggat 60

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agttgtctca tcattggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120
ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
ccatggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236
                                Met Gln Gly
                                -30
act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
                                -25                                -20                                -15
aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
                                -10                                -5                                1
aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
                                5                                10                                15
cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
20                                25                                30                                35
gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
                                40                                45                                50
gtt cct ttc tcc gaa ctg aaa gac a 501
Val Pro Phe Ser Glu Leu Lys Asp
                                55

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<210> 44  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..33

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<400> 44
Met Gln Gly Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val
                                -30                                -25                                -20
Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu
                                -15                                -10                                -5
Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
1                                5                                10                                15
Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
                                20                                25                                30
Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
                                35                                40                                45
Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
                                50                                55

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<210> 45  
 <211> 960  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..97

<220>  
 <221> CDS  
 <222> 98..934

<220>  
 <221> 3'UTR  
 <222> 935..960

[illegible]

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<210> 46
<211> 279
<212> PRT
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<213> Homo sapiens

<400> 46

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Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys
35     40     45
Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser
50     55     60
Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu
65     70     75     80
Val Tyr His Asp Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu
85     90     95
Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys
100    105    110
Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp
115    120    125
Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala
130    135    140
Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Ser Val Gly Lys
145    150    155    160
Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro
165    170    175
Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly
180    185    190
Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln
195    200    205
Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser
210    215    220
Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp
225    230    235    240
Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys
245    250    255
Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly
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<211> 1294

<212> DNA

<213> Homo sapiens

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<222> 1..266

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<221> polyA\_site



<222> 1279..1294

<400> 47

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ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180  
ttcaatacct ggaaggaaaa acaaaataac ctcaactccg ttttgaaaaa aacattccaa 240  
gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293  
Met Ile Tyr Thr Met Lys Lys Val His  
-25 -20  
gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341  
Ala Leu Trp Ala Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro  
-15 -10 -5  
ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389  
Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp  
1 5 10  
acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437  
Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys  
15 20 25 30  
gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat 485  
Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn  
35 40 45  
att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533  
Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly  
50 55 60  
aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581  
Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr  
65 70 75  
aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629  
Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys  
80 85 90  
cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677  
Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys  
95 100 105 110  
gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725  
Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu  
115 120 125  
aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773  
Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe  
130 135 140  
cag gtg gat aat tat gga acc cag ctc aat gct gtg aat aac tcc ctg 821  
Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu  
145 150 155  
act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc 869  
Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro  
160 165 170  
tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag 917  
Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu  
175 180 185 190  
aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag 965  
Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys  
195 200 205  
tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa 1013  
Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu  
210 215 220  
tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga 1061  
Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly  
225 230 235  
ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata 1109  
Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys Lys Gln Arg Val Lys Ile  
240 245 250  
gca tat gaa gaa att ttt gtt aaa aat atg tgaatttggt atagcaatgt 1159  
Ala Tyr Glu Glu Ile Phe Val Lys Asn Met

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<222> 1179..1194

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Met Pro Ser  
tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104  
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val  
-20 -15 -10 -5  
cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag 152  
Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu  
1 5 10  
ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa 200  
Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu  
15 20 25  
ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc 248  
Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu  
30 35 40  
cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta 296  
Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu  
45 50 55 60  
gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc 344  
Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala  
65 70 75  
ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac 392  
Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn  
80 85 90  
gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag 440  
Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys  
95 100 105  
gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt 488  
Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe  
110 115 120  
aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag 536  
Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu  
125 130 135 140  
gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag 584  
Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys  
145 150 155  
cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg 632  
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp  
160 165 170  
gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg 680  
Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu  
175 180 185  
cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat 728  
Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp  
190 195 200  
atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta 776  
Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu  
205 210 215 220



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<222> 1302..1317
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Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys Leu Leu Leu

cac aca att atc aca gat acg gag ttg cca cca ctg aaa ctt atg cat 442  
 His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys Leu Met His  
 10 15 20

aaa aga ttt ttc ttc aat att ttc act cga cag tgc gaa gaa ttt ata 538  
Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile

				45				50					55				
tat	ggg	gga	tgt	gaa	gga	aat	cag	aat	cga	ttt	gaa	agt	ctg	gaa	gag		586
Tyr	Gly	Gly	Cys	Glu	Gly	Asn	Gln	Asn	Arg	Phe	Glu	Ser	Leu	Glu	Glu		
			60					65					70				
tgc	aaa	aaa	atg	tgt	aca	aga	gaa	aag	cca	gat	ttc	tgc	ttt	ttg	gaa		634
Cys	Lys	Lys	Met	Cys	Thr	Arg	Glu	Lys	Pro	Asp	Phe	Cys	Phe	Leu	Glu		
			75					80					85				
gaa	gat	cct	gga	ata	tgt	cga	ggg	tat	att	acc	agg	tat	ttt	tat	aac		682
Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr	Phe	Tyr	Asn		
			90					95					100				
aat	cag	aca	aaa	cag	tgt	gaa	cgt	ttc	aag	tat	ggg	gga	tgc	ctg	ggc		730
Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly	Cys	Leu	Gly		
					110					115					120		
aat	atg	aac	aat	ttt	gag	aca	ctg	gaa	gaa	tgc	aag	aac	att	tgt	gaa		778
Asn	Met	Asn	Asn	Phe	Glu	Thr	Leu	Glu	Glu	Cys	Lys	Asn	Ile	Cys	Glu		
					125					130					135		
gat	ggg	ccg	aat	ggg	ttc	cag	gtg	gat	aat	tat	gga	acc	cag	ctc	aat		826
Asp	Gly	Pro	Asn	Gly	Phe	Gln	Val	Asp	Asn	Tyr	Gly	Thr	Gln	Leu	Asn		
			140					145					150				
gct	gtg	aat	aac	tcc	ctg	act	ccg	caa	tca	acc	aag	gtt	ccc	agc	ctt		874
Ala	Val	Asn	Asn	Ser	Leu	Thr	Pro	Gln	Ser	Thr	Lys	Val	Pro	Ser	Leu		
			155					160					165				
ttt	gaa	ttt	cac	ggg	ccc	tca	tgg	tgt	ctc	act	cca	gca	gac	aga	gga		922
Phe	Glu	Phe	His	Gly	Pro	Ser	Trp	Cys	Leu	Thr	Pro	Ala	Asp	Arg	Gly		
			170				175						180				
ttg	tgt	cgt	gcc	aat	gag	aac	aga	ttc	tac	tac	aat	tca	gtc	att	ggg		970
Leu	Cys	Arg	Ala	Asn	Glu	Asn	Arg	Phe	Tyr	Tyr	Asn	Ser	Val	Ile	Gly		
					190					195					200		
aaa	tgc	cgc	cca	ttt	aag	tac	agt	gga	tgt	ggg	gga	aat	gaa	aac	aat		1018
Lys	Cys	Arg	Pro	Phe	Lys	Tyr	Ser	Gly	Cys	Gly	Gly	Asn	Glu	Asn	Asn		
					205				210					215			
ttt	act	tcc	aaa	caa	gaa	tgt	ctg	agg	gca	tgt	aaa	aaa	ggg	ttc	atc		1066
Phe	Thr	Ser	Lys	Gln	Glu	Cys	Leu	Arg	Ala	Cys	Lys	Lys	Gly	Phe	Ile		
			220					225					230				
caa	aga	ata	tca	aaa	gga	ggc	cta	att	aaa	acc	aaa	aga	aaa	aga	aag		1114
Gln	Arg	Ile	Ser	Lys	Gly	Gly	Leu	Ile	Lys	Thr	Lys	Arg	Lys	Arg	Lys		
			235				240						245				
aag	cag	aga	gtg	aaa	ata	gca	tat	gaa	gaa	att	ttt	gtt	aaa	aat	atg		1162
Lys	Gln	Arg	Val	Lys	Ile	Ala	Tyr	Glu	Glu	Ile	Phe	Val	Lys	Asn	Met		
			250			255					260						
tgaatttggt	atagcaatgt	aacattaatt	ctactaaata	ttttatatga	aatgtttcac												1222
tatgattttc	tattttttctt	ctaaaatgct	tttaattaat	atgttcatta	aatttttctat												1282
gcttattgta	cttgttatca	aaaaaaaaaa	aaaaaa														1317

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 <212> PRT  
 <213> Homo sapiens

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 <222> 1..28

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 -10 -5 1  
 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys  
 5 10 15 20  
 Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys  
 25 30 35  
 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu

[illegible]

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<220>
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<222> 1892..1907
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gtatctctta	ggaagcaagc	ataggaaaca	ggcccatccg	tctgcctgtt	ttgcttcctc	180
atctcacttc	tacacgaggg	tgccctgtgt	caattgctgt	tttcccctaa	agagactcct	240
ttccataagt	ttgtgaaatg	ccatcgacaa	acctgatcgc	attgcatttc	actctgctgt	300
tgagtcgatt	ttctctttat	ttatcattta	gtaactcctt	gctctacaga	gctttcacct	360
tccacatatt	tcagattcat	tctttcctta	actatgtggt	ggctacgtc	ctcactgact	420
tatcaacatg	ctaccatcat	qcacttccta	tctctattcc	tcttctttaa	at ttggttcc	480

aaatgggtca caccattatt ctgagctatt acctgcctac gcagtcctag aaagtaagtg 540  
 attcaggaaa cattcccca aagtaaagt tctcaggtaa gatcagaaga ctcccatgag 600  
 tcaactgctgc tcaggatcac atctggctcc ttgaagagtg attcatcaga ccttacatag 660  
 atcttgtcat aaaaatgaaa gaggcctcgg gggaaggtct tgggctggtg gcttctgttg 720  
 gagtcctggg ctgtgggggtg aaagccgtgg ctgtagagct tcatgcggag ttacttagct 780  
 ttgctctcct gtggacaggc catgcctgtg cctccccc aaatggcata 840  
 gatgggcctt tctcaaaaat cccactcctg gagcactggc caaaattact accatcctga 900  
 tgctgggctt gcagtccttt cctttgggaa tatgaacatg gtcaaaatta agtgaacgtg 960  
 tctttctggc tttctgtaca atggagcaga acaaagtatc aatttaacta aaatttgaac 1020  
 taaatcctct ttccagggtt gga atg cac ttc tgt gga ggc acc ttg ata tcc 1073

Met His Phe Cys Gly Gly Thr Leu Ile Ser

1 5 10  
 cca gag tgg gtg ttg act gct gcc cac tgc ttg gag aag tcc cca agg 1121  
 Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser Pro Arg

15 20 25  
 cct tca tcc tac aag gtc atc ctg ggt gca cac caa gaa gtg aat ctc 1169  
 Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val Asn Leu

30 35 40  
 gaa ccg cat gtt cag gaa ata gaa gtg tct agg ctg ttc ttg gag ccc 1217  
 Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu Glu Pro

45 50 55  
 aca cga aaa gat att gcc ttg cta aag cta agc agt cct gcc gtc atc 1265  
 Thr Arg Lys Asp Ile Ala Leu Lys Leu Ser Ser Pro Ala Val Ile

60 65 70  
 act gac aaa gta atc cca gct tgt ctg cca tcc cca aat tat gtg gtc 1313  
 Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro Asn Tyr Val Val

75 80 85 90  
 gct gac cgg acc gaa tgt ttc atc act ggc tgg gga gaa acc caa ggt 1361  
 Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly

95 100 105  
 act ttt gga gct ggc ctt ctc aag gaa gcc cag ctc cct gtg att gag 1409  
 Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu Pro Val Ile Glu

110 115 120  
 aat aaa gtg tgc aat cgc tat gag ttt ctg aat gga aga gtc caa tcc 1457  
 Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser

125 130 135  
 acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act gac agt tgc cag 1505  
 Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser Cys Gln

140 145 150  
 ggt gac agt gga ggt cct ctg gtt tgc ttc gag aag gac aaa tac att 1553  
 Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile

155 160 165 170  
 tta caa gga gtc act tct tgg ggt ctt ggc tgt gca cgc ccc aat aag 1601  
 Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys

175 180 185  
 cct ggt gtc tat gtt cgt gtt tca agg ttt gtt act tgg att gag gga 1649  
 Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu Gly

190 195 200  
 gtg atg aga aat aat taattggacg ggagacagag tgacgcactg actcacctag 1704  
 Val Met Arg Asn Asn

205

aggctggaac gtgggtaggg atttagcatg ctggaaataa ctggcagtaa tcaaacgaag 1764  
 aactgtccc cagctaccag ctatgccaaa cctcggcatt ttttgtgtta ttttctgact 1824  
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<211> 207

<212> PRT

<213> Homo sapiens

<400> 54

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			20					25					30				
Ile	Leu	Gly	Ala	His	Gln	Glu	Val	Asn	Leu	Glu	Pro	His	Val	Gln	Glu		
		35					40					45					
Ile	Glu	Val	Ser	Arg	Leu	Phe	Leu	Glu	Pro	Thr	Arg	Lys	Asp	Ile	Ala		
	50				55						60						
Leu	Leu	Lys	Leu	Ser	Ser	Pro	Ala	Val	Ile	Thr	Asp	Lys	Val	Ile	Pro		
65				70						75				80			
Ala	Cys	Leu	Pro	Ser	Pro	Asn	Tyr	Val	Val	Ala	Asp	Arg	Thr	Glu	Cys		
			85					90					95				
Phe	Ile	Thr	Gly	Trp	Gly	Glu	Thr	Gln	Gly	Thr	Phe	Gly	Ala	Gly	Leu		
		100					105						110				
Leu	Lys	Glu	Ala	Gln	Leu	Pro	Val	Ile	Glu	Asn	Lys	Val	Cys	Asn	Arg		
	115					120						125					
Tyr	Glu	Phe	Leu	Asn	Gly	Arg	Val	Gln	Ser	Thr	Glu	Leu	Cys	Ala	Gly		
	130				135						140						
His	Leu	Ala	Gly	Gly	Thr	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro		
145				150						155				160			
Leu	Val	Cys	Phe	Glu	Lys	Asp	Lys	Tyr	Ile	Leu	Gln	Gly	Val	Thr	Ser		
			165					170					175				
Trp	Gly	Leu	Gly	Cys	Ala	Arg	Pro	Asn	Lys	Pro	Gly	Val	Tyr	Val	Arg		
	180						185					190					
Val	Ser	Arg	Phe	Val	Thr	Trp	Ile	Glu	Gly	Val	Met	Arg	Asn	Asn			
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<220>  
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 <222> 795..809

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 1 5  
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 Gly Pro Gly Arg Val Gly Ala Thr Ala Gly Met Asn Gly Val Asp 25  
 10 15 20 25  
 acg tcg ctt ctc tgt gat ttg ttg cag gcc ctg acc ttc ctg acc aga 148  
 Thr Ser Leu Leu Cys Asp Leu Leu Gln Ala Leu Thr Phe Leu Thr Arg 30 35 40  
 aat gaa att ctg tgc atc cat gac acc ttc ctg aag ctc tgc cct cct 196  
 Asn Glu Ile Leu Cys Ile His Asp Thr Phe Leu Lys Leu Cys Pro Pro

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Gly Lys Tyr Tyr Lys Glu Ala Thr Leu Thr Met Asp Gln Val Ser Ser
          60          65          70
ctg cca gct ctg cgg gtc aac cct ttc aga gac cgt atc tgc aga gtg 292
Leu Pro Ala Leu Arg Val Asn Pro Phe Arg Asp Arg Ile Cys Arg Val
          75          80          85
ttc tcc cac aaa ggc atg ttc tcc ttt gag gat gtg ctg ggc atg gca 340
Phe Ser His Lys Gly Met Phe Ser Phe Glu Asp Val Leu Gly Met Ala
          90          95          100          105
tct gtg ttc agc gag cag gcc tgc cca agc ctg aag att gag tat gcc 388
Ser Val Phe Ser Glu Gln Ala Cys Pro Ser Leu Lys Ile Glu Tyr Ala
          110          115          120
ttt cgc atc tat gat ttt aat gag aat ggc ttc att gat gag gag gat 436
Phe Arg Ile Tyr Asp Phe Asn Glu Asn Gly Phe Ile Asp Glu Glu Asp
          125          130          135
ctg cag agg atc atc ctg cga ctg ctg aac agt gat gac atg tct gag 484
Leu Gln Arg Ile Ile Leu Arg Leu Leu Asn Ser Asp Asp Met Ser Glu
          140          145          150
gac ctc ctg atg gac ctc acg aac cac gtc ctg agt gag tgc gat ctg 532
Asp Leu Leu Met Asp Leu Thr Asn His Val Leu Ser Glu Ser Asp Leu
          155          160          165
gac aat gac aac atg ctg tcc ttc tca gag ttt gaa cat gca atg gcc 580
Asp Asn Asp Asn Met Leu Ser Phe Ser Glu Phe Glu His Ala Met Ala
          170          175          180          185
aag tct cca gat ttc atg aac tcc ttt cgg att cac ttc tgg gga tgc 628
Lys Ser Pro Asp Phe Met Asn Ser Phe Arg Ile His Phe Trp Gly Cys
          190          195          200
tgatgtagcg gcaaatacct gacatggcag cctcgaggga gaccacagga atcgaacccc 688
ctccagcact ggagggagct gggtttgaagt atgactttgt actgggcccc cactcacctc 748
tagaatattg tttattagat aaaagaaaaa gcttttcctt agcccgaataa aaaaaaaaaa 808
t 809

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<210> 56  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

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<400> 56
Met Leu Glu Val Ser Asp Ala Leu Gly Gly Pro Gly Arg Val Pro Gly
1          5          10          15
Ala Thr Ala Gly Met Asn Gly Val Asp Thr Ser Leu Leu Cys Asp Leu
          20          25          30
Leu Gln Ala Leu Thr Phe Leu Thr Arg Asn Glu Ile Leu Cys Ile His
          35          40          45
Asp Thr Phe Leu Lys Leu Cys Pro Pro Gly Lys Tyr Tyr Lys Glu Ala
          50          55          60
Thr Leu Thr Met Asp Gln Val Ser Ser Leu Pro Ala Leu Arg Val Asn
          65          70          75          80
Pro Phe Arg Asp Arg Ile Cys Arg Val Phe Ser His Lys Gly Met Phe
          85          90          95
Ser Phe Glu Asp Val Leu Gly Met Ala Ser Val Phe Ser Glu Gln Ala
          100          105          110
Cys Pro Ser Leu Lys Ile Glu Tyr Ala Phe Arg Ile Tyr Asp Phe Asn
          115          120          125
Glu Asn Gly Phe Ile Asp Glu Glu Asp Leu Gln Arg Ile Ile Leu Arg
          130          135          140
Leu Leu Asn Ser Asp Asp Met Ser Glu Asp Leu Leu Met Asp Leu Thr
          145          150          155          160
Asn His Val Leu Ser Glu Ser Asp Leu Asp Asn Asp Asn Met Leu Ser
          165          170          175          180
Phe Ser Glu Phe Glu His Ala Met Ala Lys Ser Pro Asp Phe Met Asn
          180          185          190

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Ser Phe Arg Ile His Phe Trp Gly Cys  
 195 200

<210> 57  
 <211> 1133  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..475

<220>  
 <221> CDS  
 <222> 476..964

<220>  
 <221> 3'UTR  
 <222> 965..1133

<220>  
 <221> polyA\_signal  
 <222> 1101..1106

<220>  
 <221> polyA\_site  
 <222> 1118..1133

<400> 57  
 gacataatca gagctatgct ggaggagaag agggcagcca tttgctggct ggcttgcaagt 60  
 gagccaggag gtggcaggac gagttaggag gctgggtcag tagctcgggc aagagcaggg 120  
 cccccccaga tctgaaggcc tcccaggccc ccaggccca gcgggtccca gaggagagcg 180  
 aggaccctaa ggtaactccg gtgagaaggc cgaccaggga tttcaaggcc agccaggctt 240  
 tccggggccca ccgggtcccc ctggattccc aggcaaagtt ggatcacctg gcccacctgg 300  
 ccctcaagca gagaagggca gcgaagggat tcgaggccca tcaggcctgc ctggctcccc 360  
 tggggccaccg ggacctcctg ggattcaggc ccccgccggg ctggatgggt tggatgggaa 420  
 ggatggcaag cctggcttga ggggggaccc tggctctgct ggccccctg gactc atg 478  
 Met  
 1  
 gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526  
 Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly  
 5 10 15  
 cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574  
 Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg  
 20 25 30  
 cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622  
 Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro  
 35 40 45  
 ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670  
 Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly  
 50 55 60 65  
 cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718  
 Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr  
 70 75 80  
 gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766  
 Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly  
 85 90 95  
 cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814  
 Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met  
 100 105 110  
 ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862  
 Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly  
 115 120 125

[illegible][illegible]

<220>  
<221> 5'UTR  
<222> 1..78

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<220>  
<221> 3'UTR  
<222> 643..838
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<220>
<221> polyA_site
<222> 823..838
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<400> 59															60
aaagactgcg tgcagaaggt gactgtctca gtggagctgg gtcattctcag gccttggctc															111
cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg															
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met															
1 5 10															
aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat															159
Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp															
15 20 25															
aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tcg agc ctg															207
Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu															
30 35 40															
gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg															255
Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala															
45 50 55															
gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa															303
Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys															
60 65 70 75															
gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat															351
Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp															
80 85 90															
gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag															399
Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys															
95 100 105															
gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg															447
Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp															
110 115 120															
cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat															495
His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His															
125 130 135															
gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg															543
Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu															
140 145 150 155															
tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg															591
Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly															
160 165 170															
gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca															639
Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser															
175 180 185															
aaa tgaagatact gacaccacct ttgccctccc cgtcaccgcg caccaccct															692
Lys															
gacccctccc tcagctgtcc tgtgccccgc cctctccgc acactcagtc ccctgctg															752
gcgttctctgc cgcagctctg acctggtgct gtgcacctgg catcttaata aamcctgctt															812
atacttccct aaaaaaaaaa aaaaaa															838

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<210> 60
<211> 188
<212> PRT
<213> Homo sapiens
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<400>	60															
Met	Cys	Phe	Pro	Lys	Val	Leu	Ser	Asp	Asp	Met	Lys	Lys	Leu	Lys	Ala	
1				5					10					15		
Arg	Met	His	Gln	Ala	Ile	Glu	Arg	Phe	Tyr	Asp	Lys	Met	Gln	Asn	Ala	
			20					25					30			
Glu	Ser	Gly	Arg	Gly	Gln	Val	Met	Ser	Ser	Leu	Ala	Glu	Leu	Glu	Asp	
		35					40					45				
Asp	Phe	Lys	Glu	Gly	Tyr	Leu	Glu	Thr	Val	Ala	Ala	Tyr	Tyr	Glu	Glu	
	50					55					60					
Gln	His	Pro	Glu	Leu	Thr	Pro	Leu	Leu	Glu	Lys	Glu	Arg	Asp	Gly	Leu	
65					70					75					80	
Arg	Cys	Arg	Gly	Asn	Arg	Ser	Pro	Val	Pro	Asp	Val	Glu	Asp	Pro	Ala	
				85					90					95		

Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe  
 100 105 110  
 Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala  
 115 120 125  
 Trp Val Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu  
 130 135 140  
 Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met  
 145 150 155 160  
 Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu  
 165 170 175  
 Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys  
 180 185

<210> 61  
 <211> 862  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..158

<220>  
 <221> CDS  
 <222> 159..764

<220>  
 <221> 3'UTR  
 <222> 765..862

<400> 61  
 attttttttt ttggcacgcc tgcagccaag ttggggaggg tttcctggac agaggtcctt 60  
 tggctgctgc cttaagacgt gcagcctggg ccgtggctgt cactgcgttc ggaccagac 120  
 ccgctgcagg cagcagcagc ccccgcccgcc gcagcagc atg gag ctc tgg ggg gcc 176  
 Met Glu Leu Trp Gly Ala  
 -20 -15  
 tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224  
 Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Thr Glu  
 -10 -5 1  
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272  
 Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val  
 5 10 15  
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320  
 Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu  
 20 25 30  
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368  
 Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val  
 35 40 45 50  
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416  
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr  
 55 60 65  
 cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tcg cgc ggg 464  
 Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly  
 70 75 80  
 ggc acc ctg agc acc cct cag act ggc tcg gag aac gac gcc ctg tat 512  
 Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr  
 85 90 95  
 gag tac ctg cgc cag agc gtg ggc aac gag gcc gag atc tgg ctg ggc 560  
 Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly  
 100 105 110  
 ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc 608  
 Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala  
 115 120 125 130

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cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
      135      140      145
ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
      150      155      160
aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
      165      170      175
ttc ggc atc gtg tagccggcgg ggcggggggcc gtggggggggcc tggaggagggg 804
Phe Gly Ile Val
      180
caggagccgc gggaggccgg gaggagggtg gggaccttgc agcccccatc ctctccgt 862

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<210> 62  
 <211> 202  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..21

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<400> 62
Met Glu Leu Trp Gly Ala Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu
  -20      -15      -10
Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val
  -5      1      5      10
Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
      15      20      25
Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
      30      35      40
Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys
      45      50      55
Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu
      60      65      70      75
Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser
      80      85      90
Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu
      95      100      105
Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp
      110      115      120
Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu
      125      130      135
Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu
      140      145      150      155
Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln
      160      165      170
Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val
      175      180

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<210> 63  
 <211> 618  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..194

<220>  
 <221> CDS  
 <222> 195..587

<220>  
 <221> 3'UTR  
 <222> 588..618

<220>  
 <221> polyA\_signal  
 <222> 578..583

<220>  
 <221> polyA\_site  
 <222> 604..618

<400> 63  
 atttgcttag gtctgatcaa tctgctccac acaatttctc agtgatcctc tgcattctctg 60  
 cctacaaggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120  
 ttcgttttac cttgatctct ctctgacaaa gaaatccaga tgatgcgaga cctgatgaag 180  
 acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230  
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu  
 -20 -15 -10  
 act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278  
 Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala  
 -5 1 5  
 cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326  
 Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln  
 10 15 20  
 agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374  
 Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala  
 25 30 35  
 tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422  
 Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr  
 40 45 50 55  
 aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470  
 Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser  
 60 65 70  
 atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518  
 Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg  
 75 80 85  
 act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566  
 Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met  
 90 95 100  
 tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618  
 Cys Phe Ala Leu Leu Asn Cys  
 105 110

<210> 64  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..22

<400> 64  
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly  
 -20 -15 -10  
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln  
 -5 1 5 10  
 Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu  
 15 20 25  
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln  
 30 35 40







<220>  
 <221> CDS  
 <222> 63..572

<220>  
 <221> 3'UTR  
 <222> 573..789

<220>  
 <221> polyA\_signal  
 <222> 750..755

<220>  
 <221> polyA\_site  
 <222> 774..789

<400> 67  
 atatgtcatc agggcccccg cctgggaggt gtgctgccag agattttgcc tcttcaaggt 60  
 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107  
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly  
 1 5 10 15  
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155  
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys  
 20 25 30  
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203  
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu  
 35 40 45  
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251  
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu  
 50 55 60  
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299  
 Val Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro  
 65 70 75  
 ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347  
 Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val  
 80 85 90 95  
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395  
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu  
 100 105 110  
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443  
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile  
 115 120 125  
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491  
 Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr  
 130 135 140  
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539  
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro  
 145 150 155  
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592  
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp  
 160 165 170  
 gaggagggac gcccagggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652  
 caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712  
 aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772  
 gaaaaaaaa aaaaaaa 789

<210> 68  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 68

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Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
1      5      10      15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
20      25      30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
35      40      45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
50      55      60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65      70      75      80
Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
85      90      95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
100     105     110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
115     120     125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130     135     140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145     150     155     160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
165     170

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<210> 69  
 <211> 2556  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..66  
 <220>  
 <221> CDS  
 <222> 67..2427

<220>  
 <221> 3'UTR  
 <222> 2428..2556

<220>  
 <221> polyA\_signal  
 <222> 2522..2527

<220>  
 <221> polyA\_site  
 <222> 2541..2556

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<400> 69
gtccccgcgt ccttggaat tcccgacttc ccaacgggtt cctgctggca gccccgaagc 60
cgccacc atg ttc cgc ctc tgg ttg ctg ctg gcc ggg ctc tgc ggc ctc 108
      Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu
      -15      -10      -5
ctg gcg tca aga ccc ggt ttt caa aat tca ctt cta cag atc gta att 156
Leu Ala Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile
1      5      10      15
cca gag aaa atc caa aca aat aca aat gac agt tca gaa ata gaa tat 204
Pro Glu Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr
20      25      30
gaa caa ata tcc tat att att cca ata gat gag aaa ctg tac act gtg 252
Glu Gln Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val
35      40      45
cac ctt aaa caa aga tat ttt tta aca gat aat ttt atg atc tat ttg 300

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His	Leu	Lys	Gln	Arg	Tyr	Phe	Leu	Thr	Asp	Asn	Phe	Met	Ile	Tyr	Leu	
		50					55					60				
tac	aat	caa	gga	tct	atg	aat	act	tat	tct	tca	gat	att	cag	act	caa	348
Tyr	Asn	Gln	Gly	Ser	Met	Asn	Thr	Tyr	Ser	Ser	Asp	Ile	Gln	Thr	Gln	
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Cys	Tyr	Tyr	Gln	Gly	Asn	Ile	Glu	Glu	Tyr	Pro	Asp	Ser	Met	Val	Thr	
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Leu	Ser	Thr	Cys	Ser	Gly	Leu	Arg	Gly	Ile	Leu	Gln	Phe	Glu	Asn	Val	
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Ser	Tyr	Gly	Ile	Glu	Pro	Leu	Glu	Ser	Ala	Val	Glu	Phe	Gln	His	Val	
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Leu	His	Lys	Leu	Lys	Asn	Glu	Asp	Asn	Asp	Ile	Ala	Ile	Phe	Ile	Asp	
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Arg	Ser	Leu	Lys	Glu	Gln	Pro	Met	Asp	Asp	Asn	Ile	Phe	Ile	Ser	Glu	
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Lys	Ser	Glu	Pro	Ala	Val	Pro	Asp	Leu	Phe	Pro	Leu	Tyr	Leu	Glu	Met	
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cat	att	gtg	gtg	gac	aaa	act	ttg	tat	gat	tac	tgg	ggc	tct	gat	agc	684
His	Ile	Val	Val	Asp	Lys	Thr	Leu	Tyr	Asp	Tyr	Trp	Gly	Ser	Asp	Ser	
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Trp	Ser	Asp	Glu	Asn	Lys	Ile	Ser	Thr	Val	Gly	Glu	Ala	Asp	Glu	Leu	
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Leu	Gln	Lys	Phe	Leu	Glu	Trp	Lys	Gln	Ser	Tyr	Leu	Asn	Leu	Arg	Pro	
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His	Asp	Ile	Ala	Tyr	Leu	Leu	Ile	Tyr	Met	Asp	Tyr	Pro	Arg	Tyr	Leu	
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Gly	Ala	Val	Phe	Pro	Gly	Thr	Met	Cys	Ile	Thr	Arg	Tyr	Ser	Ala	Gly	
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Val	Ala	Leu	Tyr	Pro	Lys	Glu	Ile	Thr	Leu	Glu	Ala	Phe	Ala	Val	Ile	
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Val	Thr	Gln	Met	Leu	Ala	Leu	Ser	Leu	Gly	Ile	Ser	Tyr	Asp	Asp	Pro	
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Lys	Lys	Cys	Gln	Cys	Ser	Glu	Ser	Thr	Cys	Ile	Met	Asn	Pro	Glu	Val	
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Val	Gln	Ser	Asn	Gly	Val	Lys	Thr	Phe	Ser	Ser	Cys	Ser	Leu	Arg	Ser	
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Phe	Gln	Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys	
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cca	caa	atg	caa	aaa	aaa	tct	ccg	aaa	cca	gtc	tgt	ggc	aat	ggc	aga	1260
Pro	Gln	Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg	
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Leu	Glu	Gly	Asn	Glu	Ile	Cys	Asp	Cys	Gly	Thr	Glu	Ala	Gln	Cys	Gly		
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Pro	Ala	Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala		
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aaa	tgt	tat	aaa	gga	ctg	tgc	tgc	aaa	gac	tgt	caa	att	tta	caa	tca	1404	
Lys	Cys	Tyr	Lys	Gly	Leu	Cys	Cys	Lys	Asp	Cys	Gln	Ile	Leu	Gln	Ser		
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Gly	Val	Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu		
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Asn	Gly	Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp		
		465				470				475							
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Cys	His	Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser		
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Arg	Phe	Gly	Asn	Cys	Gly	Arg	Asp	Arg	Asn	Asn	Lys	Tyr	Val	Phe	Cys		
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Gly	Trp	Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr		
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Arg	Lys	Pro	Phe	His	Gln	Glu	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val		
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Arg	Asp	Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val		
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Pro	Asp	Pro	Leu	Ala	Val	Lys	Asn	Gly	Ser	Gln	Cys	Asp	Ile	Gly	Arg		
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gtt	tgt	gta	aat	cgt	gaa	tgt	gta	gaa	tca	agg	ata	att	aag	gct	tca	1932	
Val	Cys	Val	Asn	Arg	Glu	Cys	Val	Glu	Ser	Arg	Ile	Ile	Lys	Ala	Ser		
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Ala	His	Val	Cys	Ser	Gln	Gln	Cys	Ser	Gly	His	Gly	Val	Cys	Asp	Ser		
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Ile	Arg	Ser	Lys	Gly	Phe	Ser	Ile	Phe	Pro	Glu	Glu	Asp	Met	Gly	Ser		
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Ile	Met	Glu	Arg	Ala	Ser	Gly	Lys	Thr	Glu	Asn	Thr	Trp	Leu	Leu	Gly		
				660					665					670			
ttc	ctc	att	gct	ctt	cct	att	ctc	att	gta	aca	acc	gca	ata	gtt	ttg	2172	
Phe	Leu	Ile	Ala	Leu	Pro	Ile	Leu	Ile	Val	Thr	Thr	Ala	Ile	Val	Leu		
			675					680					685				
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Ala	Arg	Lys	Gln	Leu	Lys	Asn	Trp	Phe	Ala	Lys	Glu	Glu	Glu	Phe	Pro		
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agt	agc	gaa	tct	aaa	tcg	gaa	ggc	agc	aca	cag	aca	tat	gcc	agc	caa	2268	
Ser	Ser	Glu	Ser	Lys	Ser	Glu	Gly	Ser	Thr	Gln	Thr	Tyr	Ala	Ser	Gln		
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Gln Met Leu Ala Leu Ser	Leu Gly Ile Ser Tyr Asp Asp Pro Lys Lys			
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Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val Val Gln				
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Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser Phe Gln				
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Asn Phe Ile Ser Asn Val Gly Val Lys Cys Leu Gln Asn Lys Pro Gln				
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Met Gln Lys Lys Ser Pro Lys Pro Val Cys Gly Asn Gly Arg Leu Glu				
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Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala Gln Cys Gly Pro Ala				
385			395	400
Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala Lys Cys				
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Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser Gly Val				
	420		425	430
Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu Asn Cys				
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Asn Gly Ser Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile Asn Gly				
	450		455	460
Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp Cys His				
465			475	480
Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser Arg Asn				
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Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp Arg Phe				
	500		505	510
Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp				
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Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr Arg Lys				
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Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp				
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Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val Pro Asp				
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Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg Val Cys				
	580		585	590
Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser Ala His				
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Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser Arg Asn				
	610		615	620
Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln Ile Arg				
625			635	640
Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser Ile Met				
	645		650	655
Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly Phe Leu				
	660		665	670
Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu Ala Arg				
	675		680	685
Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro Ser Ser				
	690		695	700
Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser				
705			715	720
Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser Glu Ser				
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Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu				
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Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser				
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 Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro  
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 cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc 145  
 His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu  
           15                  20                  25                  30  
 ctg tac ctc tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata 193  
 Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile  
                   35                  40                  45  
 gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241  
 Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val  
                   50                  55                  60  
 cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289  
 Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu  
           65                  70                  75  
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 Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu  
           80                  85                  90  
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 Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Leu Ser Met Phe His  
           95                  100                  105                  110  
 gtc tcc acg cca ctg cca gtg atg acc ggt ggt ttc ctg agc tgc atc 433  
 Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile  
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 Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val  
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 ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gst gca 529  
 Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala  
           145                  150                  155  
 ctc ctg gct gca atg ctt cgg ggg ctg gca ggg ggc cga gtc ctg gcc 577  
 Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala  
           160                  165                  170  
 ctc ctg gag gag aac tcc aca ccc cag cta gca ggg atc ctg gcc cgg 625  
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Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro  
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Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln  
35 40 45  
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu  
50 55 60  
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly  
65 70 75 80  
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Met Met Gly Val Phe Val Val Ala Ala  
1 5  
aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162

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Ala	Thr	Asp	Leu	Ser	Glu	Phe	Ala	Ala	Lys	Ala	Ala	Leu	Ser	Ala	Gly	
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aaa	gtc	tca	cct	gaa	aca	ggt	gac	agt	gtg	att	atg	ggc	aat	gtc	ctg	258
Lys	Val	Ser	Pro	Glu	Thr	Val	Asp	Ser	Val	Ile	Met	Gly	Asn	Val	Leu	
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cag	agt	tct	tca	gat	gct	ata	tat	ttg	gca	agg	cat	gtt	ggg	ttg	cgt	306
Gln	Ser	Ser	Ser	Asp	Ala	Ile	Tyr	Leu	Ala	Arg	His	Val	Gly	Leu	Arg	
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Val	Gly	Ile	Pro	Lys	Glu	Thr	Pro	Ala	Leu	Thr	Ile	Asn	Arg	Leu	Cys	
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ggg	tct	ggg	ttt	cag	tcc	att	gtg	aat	gga	tgt	cag	gaa	att	tgt	gtt	402
Gly	Ser	Gly	Phe	Gln	Ser	Ile	Val	Asn	Gly	Cys	Gln	Glu	Ile	Cys	Val	
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Lys	Glu	Ala	Glu	Val	Val	Leu	Cys	Gly	Gly	Thr	Glu	Ser	Met	Ser	Gln	
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gct	ccc	tac	tgt	gtc	aga	aat	gtg	cgt	ttt	gga	acc	aag	ctt	gga	tca	498
Ala	Pro	Tyr	Cys	Val	Arg	Asn	Val	Arg	Phe	Gly	Thr	Lys	Leu	Gly	Ser	
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Asp	Ile	Lys	Leu	Glu	Asp	Ser	Leu	Trp	Val	Ser	Leu	Thr	Asp	Gln	His	
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Val	Gln	Leu	Pro	Met	Ala	Met	Thr	Ala	Glu	Asn	Leu	Ala	Val	Lys	His	
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Arg	Trp	Lys	Ala	Ala	Asn	Asp	Ala	Gly	Tyr	Phe	Asn	Asp	Glu	Met	Ala	
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Pro	Ile	Glu	Val	Lys	Thr	Lys	Lys	Gly	Lys	Gln	Thr	Met	Gln	Val	Asp	
					205			210					215			
gag	cat	gct	cgg	ccc	caa	acc	acc	ctg	gaa	cag	tta	cag	aaa	ctt	cct	786
Glu	His	Ala	Arg	Pro	Gln	Thr	Thr	Leu	Glu	Gln	Leu	Gln	Lys	Leu	Pro	
					220		225					230				
cca	gta	ttc	aag	aaa	gat	gga	act	gtt	act	gca	ggg	aat	gca	tcg	ggg	834
Pro	Val	Phe	Lys	Lys	Asp	Gly	Thr	Val	Thr	Ala	Gly	Asn	Ala	Ser	Gly	
					235		240				245					
gta	gct	gat	ggg	gct	gga	gct	gtt	atc	ata	gct	agt	gaa	gat	gct	gtt	882
Val	Ala	Asp	Gly	Ala	Gly	Ala	Val	Ile	Ile	Ala	Ser	Glu	Asp	Ala	Val	
					250		255			260					265	
aag	aaa	cat	aac	ttc	aca	cca	ctg	gca	aga	att	gtg	ggc	tac	ttt	gta	930
Lys	Lys	His	Asn	Phe	Thr	Pro	Leu	Ala	Arg	Ile	Val	Gly	Tyr	Phe	Val	
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tct	gga	tgt	gat	ccc	tct	atc	atg	ggg	att	ggg	cct	gtc	cct	gct	atc	978
Ser	Gly	Cys	Asp	Pro	Ser	Ile	Met	Gly	Ile	Gly	Pro	Val	Pro	Ala	Ile	
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Ser	Gly	Ala	Leu	Lys	Lys	Ala	Gly	Leu	Ser	Leu	Lys	Asp	Met	Asp	Leu	
					300		305					310				
gta	gag	gtg	aat	gaa	gct	ttt	gct	ccc	cag	tac	ttg	gct	gtt	gag	agg	1074
Val	Glu	Val	Asn	Glu	Ala	Phe	Ala	Pro	Gln	Tyr	Leu	Ala	Val	Glu	Arg	
					315		320				325					
agt	ttg	gat	ctt	gac	ata	agt	aaa	acc	aat	gtg	aat	gga	gga	gcc	att	1122
Ser	Leu	Asp	Leu	Asp	Ile	Ser	Lys	Thr	Asn	Val	Asn	Gly	Gly	Ala	Ile	
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gct	ttg	ggg	cac	cca	ctg	gga	gga	tct	gga	tca	aga	att	act	gca	cac	1170



Ala Pro Gln Tyr Leu Ala Val Glu Arg Ser Leu Asp Leu Asp Ile Ser  
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 Lys Thr Asn Val Asn Gly Gly Ala Ile Ala Leu Gly His Pro Leu Gly  
 340 345 350  
 Gly Ser Gly Ser Arg Ile Thr Ala His Leu Val His Glu Leu Arg Arg  
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 370 375 380  
 Gly Ile Ala Val Ile Ile Gln Ser Thr Ala  
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<220>  
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 -5 1 5 10  
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 Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser  
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 gcc aca gag gtc aca ggg cac cgc tgg ctg aag ggg ggc gtg gtg ctg 254  
 Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu  
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 Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser  
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 Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val  
 75 80 85 90  
 aag tcg tca gaa cac atc aac gag ggg gag acg gcc atg ctg gtc tgc 446  
 Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys  
 95 100 105  
 aag tca gag tcc gtg cca cct gtc act gac tgg gcc tgg tac aag atc 494

Lys	Ser	Glu	Ser	Val	Pro	Pro	Val	Thr	Asp	Trp	Ala	Trp	Tyr	Lys	Ile	
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Thr	Asp	Ser	Glu	Asp	Lys	Ala	Leu	Met	Asn	Gly	Ser	Glu	Ser	Arg	Phe	
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Phe	Val	Ser	Ser	Ser	Gln	Gly	Leu	Ser	Glu	Leu	His	Ile	Glu	Asn	Leu	
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aac	atg	gag	gcc	gac	ccc	ggc	cag	tac	cgg	tgc	aac	ggc	acc	agc	tcc	638
Asn	Met	Glu	Ala	Asp	Pro	Gly	Gln	Tyr	Arg	Cys	Asn	Gly	Thr	Ser	Ser	
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aag	ggc	tcc	gac	cag	gcc	atc	atc	acg	ctc	cgc	gtg	cgc	agc	cac	ctg	686
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gcc	gcc	ctc	tgg	ccc	ttc	ctg	ggc	atc	gtg	gct	gag	gtg	ctg	gtg	ctg	734
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		190					195						200			
gtc	acc	atc	atc	ttc	atc	tac	gag	aag	cgc	cgg	aag	ccc	gag	gac	gtc	782
Val	Thr	Ile	Ile	Phe	Ile	Tyr	Glu	Lys	Arg	Arg	Lys	Pro	Glu	Asp	Val	
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Leu	Asp	Asp	Asp	Asp	Ala	Gly	Ser	Ala	Pro	Leu	Lys	Ser	Ser	Gly	Gln	
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cac	cag	aat	gac	aaa	ggc	aag	aac	gtc	cgc	cag	agg	aac	tct	tcc		875
His	Gln	Asn	Asp	Lys	Gly	Lys	Asn	Val	Arg	Gln	Arg	Asn	Ser	Ser		
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cgtctgtggc	tttcagcctc				tggtctctgag			tcatgtgccg			gtgggcggca			cagccttctc		1175
catctggccg	agtcagtgcc				aggtcccttgc			cctttgtgga			aagtccacagg			tcacacgagg		1235
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<213> Homo sapiens
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Leu	Gly	Ser	Lys	Ile	Leu	Leu	Thr	Cys	Ser	Leu	Asn	Asp	Ser	Ala	Thr	
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Glu	Val	Thr	Gly	His	Arg	Trp	Leu	Lys	Gly	Gly	Val	Val	Leu	Lys	Glu	
		30					35					40				
Asp	Ala	Leu	Pro	Gly	Gln	Lys	Thr	Glu	Phe	Lys	Val	Asp	Ser	Asp	Asp	
	45					50					55					
Gln	Trp	Gly	Glu	Tyr	Ser	Cys	Val	Phe	Leu	Pro	Glu	Pro	Met	Gly	Thr	
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Ala	Asn	Ile	Gln	Leu	His	Gly	Pro	Pro	Arg	Val	Lys	Ala	Val	Lys	Ser	



				80					85					90		
Ser	Glu	His	Ile	Asn	Glu	Gly	Glu	Thr	Ala	Met	Leu	Val	Cys	Lys	Ser	
			95					100					105			
Glu	Ser	Val	Pro	Pro	Val	Thr	Asp	Trp	Ala	Trp	Tyr	Lys	Ile	Thr	Asp	
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Ser	Glu	Asp	Lys	Ala	Leu	Met	Asn	Gly	Ser	Glu	Ser	Arg	Phe	Phe	Val	
	125					130					135					
Ser	Ser	Ser	Gln	Gly	Leu	Ser	Glu	Leu	His	Ile	Glu	Asn	Leu	Asn	Met	
140					145					150					155	
Glu	Ala	Asp	Pro	Gly	Gln	Tyr	Arg	Cys	Asn	Gly	Thr	Ser	Ser	Lys	Gly	
			160						165					170		
Ser	Asp	Gln	Ala	Ile	Ile	Thr	Leu	Arg	Val	Arg	Ser	His	Leu	Ala	Ala	
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Leu	Trp	Pro	Phe	Leu	Gly	Ile	Val	Ala	Glu	Val	Leu	Val	Leu	Val	Thr	
		190					195					200				
Ile	Ile	Phe	Ile	Tyr	Glu	Lys	Arg	Arg	Lys	Pro	Glu	Asp	Val	Leu	Asp	
	205					210					215					
Asp	Asp	Asp	Ala	Gly	Ser	Ala	Pro	Leu	Lys	Ser	Ser	Gly	Gln	His	Gln	
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tctttcggac	tcgaatcacg	gctgctgcga	agggctctagt	tccggacact	agggtgcccg	300						
aacgcgctga	tgccccgagt	gctcgcaggg	cttcccgccta	acc atg ctg ccg ccg		355						
				Met Leu Pro Pro								
ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc ctg cta ctg ctg						403						
Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu Leu Leu Leu Leu												
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gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca tcc cca ggc cca						451						
Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro Ser Pro Gly Pro												
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gat tac ctg cgg cgc ggc tgg atg cgg ctg cta gcg gag ggc gag ggc						499						
Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala Glu Gly Glu Gly												
	10		15		20							
tgc gct ccc tgc cgg cca gaa gag tgc gcc gcg ccg cgg ggc tgc ctg						547						
Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro Arg Gly Cys Leu												
	25		30		35							
ggc ggc agg gtg cgc gac gcg tgc ggc tgc tgc tgg gaa tgc gcc aac						595						
Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp Glu Cys Ala Asn												
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ctc qaq qqc caq ctc tgc gac ctg gac ccc agt gct cac ttc tac ggg						643						



His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr  
70 75 80  
Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys  
85 90 95  
Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln  
100 105 110  
Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu  
115 120 125 130  
Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser  
135 140 145  
His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly  
150 155 160  
Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp  
165 170 175  
Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln  
180 185 190  
Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile  
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Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro  
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Ile Leu Ser Gly Gly Glu Ser Thr Glu Ile Pro Pro Tyr Val Met Lys  
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Cys Pro Ser Asn Gly Leu Cys Ser Arg Leu Pro Ala Asp Cys Ile Asp  
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Cys Thr Thr Asn Phe Ser Cys Thr Tyr Gly Lys Pro Val Thr Phe Asp

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Cys Ala Val Lys Pro Ser Val Thr	Cys Val Asp Gln Asp Phe Lys Ser		
45	50	55	
caa aag aac ttc atc att aac atg act	tgc aga ttt tgc tgg cag ctt	341	
Gln Lys Asn Phe Ile Ile Asn Met Thr	Cys Arg Phe Cys Trp Gln Leu		
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cct gaa aca gat tac gag tgt acc aac tcc	acc agc tgc atg acg gtg	389	
Pro Glu Thr Asp Tyr Glu Cys Thr Asn Ser	Thr Ser Cys Met Thr Val		
75	80	85	90
tcc tgt cct cgg cag cgc tac cct gcc aac	tgc acg gtg cgg gac cac	437	
Ser Cys Pro Arg Gln Arg Tyr Pro Ala Asn	Cys Thr Val Arg Asp His		
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Val His Cys Leu Gly Asn Arg Thr Phe Pro	Lys Met Leu Tyr Cys Asn		
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tgg act gga ggc tat aag tgg tct acg gct	ctg gct cta agc atc acc	533	
Trp Thr Gly Tyr Lys Trp Ser Thr Ala Leu	Ala Leu Ser Ile Thr		
125	130	135	
ctc ggt ggg ttt gga gca gac cgt ttc tac	ctg ggc cag tgg cgg gaa	581	
Leu Gly Gly Phe Gly Ala Asp Arg Phe Tyr	Leu Gly Gln Trp Arg Glu		
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ggc ctc ggc aag ctc ttc agc ttc ggt ggc	ctg gga ata tgg acg ctg	629	
Gly Leu Gly Lys Leu Phe Ser Phe Gly Gly	Gly Ile Trp Thr Leu		
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ata gac gtc ctg ctc att gga gtt ggc tat	ggt gga cca gca gat ggc	677	
Ile Asp Val Leu Leu Ile Gly Val Gly Tyr	Val Gly Pro Ala Asp Gly		
175	180	185	
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Ser Leu Tyr Ile			
190			
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 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu  
 75 80 85  
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501  
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro  
 90 95 100 105  
 ggc ccc agc tgaccgcccc agccccgcgt gattgcacct gtctgcattc 550  
 Gly Pro Ser  
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 45 50 55  
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
 60 65 70  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu  
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 90 95 100  
 Gly Pro Ser  
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<210> 85

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 <213> Homo sapiens

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 <222> 511..1754

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 <222> 1718..1723

<220>  
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 <222> 1739..1754

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 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg 165  
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu  
 -20 -15 -10  
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213  
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro  
 -5 1 5  
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261  
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala  
 10 15 20 25  
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309  
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu  
 30 35 40  
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357  
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe  
 45 50 55  
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405  
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
 60 65 70  
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu  
 75 80 85  
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501  
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro  
 90 95 100 105  
 ggc ccc agc tgaccgcccc agccccgcgt gattgcacct gtctgcattc 550  
 Gly Pro Ser  
 acagacattc gggagacggc cttcgtgttc gccatcactg cggccggcgc cagccacgcc 610  
 gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670  
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 accgagtgca aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970  
 ctgcctccat ttgcgcaggt gggcgcgcggt ctgctggagc gcttycacgg cgcctcacgc 1030  
 gtcacgggca ccaacgacgg caaggccctg ctgccccgcg tccgcacgct caagccgcgc 1090  
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<221> polyA\_site

<222> 1416..1431

<400> 87

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gccccaaacca aggccccag agagggtcccc caggccccctt tgggtccctg agcctcagct 120  
ggagatccgg cgaggagac caacgcctgc c atg ctg ttc cgg ctg tca gag 172  
Met Leu Phe Arg Leu Ser Glu

1 5  
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220  
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly

10 15 20  
gag ggg cac cat ctg aag tgc aag aga ccc aac ccc tgt gcc tac aca 268  
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr

25 30 35  
cca cct tgc ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316  
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln

40 45 50 55  
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364  
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu

60 65 70  
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412  
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu

75 80 85  
gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460  
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala

90 95 100  
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508  
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys

105 110 115  
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556  
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu

120 125 130 135  
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604  
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu

140 145 150  
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652  
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly

155 160 165  
aca taggcacca gcctgcatct cccaggagga agtggagggg acatcgctgt 705  
Thr

tccccagaaa cccactctat cctcacctgt ttttgtgtc ttccctctgc ctgctagggc 765

tgcggcttct gacttctaga agactaaggc tgggtctgtgt ttgcttgttt gcccaccttt 825

ggctgatacc cagagaacct gggcacttgc tgcttgatgc ccaccctgc cagtcattcc 885

tccattcacc cagcgggagg tgggatgtga gacagcccac attggaaaat ccagaaaacc 945

gggaacaggg atttgccctt cacaattcta ctccccagat cctctccctt ggacacagga 1005

gaccacaggg gcaggaccct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065

cttagatcct tttctacca ctttctatg gaggattcca agtcaccact tctctaccg 1125

gcttctacca ggggtccagga ctaaggcggt tttctccata gcctcaacat tttgggaatc 1185

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acagcggggg gcgccaggtt ttccttgctc cccagctgct ctgccccctt ccccttcttc 1365

cctgactcca ggccctgaacc cctcccgctg tgtaataaat ctttgtaaag aaaaaaaaaa 1425

aaaaaa 1431

<210> 88

<211> 168

<212> PRT

<213> Homo sapiens

<400> 88

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 35 40 45  
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln  
 50 55 60  
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr  
 65 70 75 80  
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu  
 85 90 95  
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser  
 100 105 110  
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu  
 115 120 125  
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp  
 130 135 140  
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg  
 145 150 155 160  
 Pro Ser Pro Ser Glu Pro Gly Thr  
 165

<210> 89  
 <211> 1431  
 <212> DNA  
 <213> Homo sapiens

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 <222> 1399..1404

<220>  
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 <222> 1416..1431

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 ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172  
 Met Leu Phe Arg Leu Ser Glu  
 1 5  
 cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220  
 His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly  
 10 15 20  
 gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268  
 Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr  
 25 30 35  
 cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316  
 Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln  
 40 45 50 55  
 tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364  
 Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu

ctg ggg gag	60	ctt cgg gag	ctg ggt	tat cca aga	gag gaa	gat gag	gag	412
Leu Gly Glu	Leu Arg Glu	Leu Gly Tyr	Pro Arg Glu	Glu Glu Asp	Glu Glu			
	75		80		85			
gaa gag gag	gat gat	gaa gaa	gag gaa	gaa gaa	gag gac	agc cag	gct	460
Glu Glu Glu	Asp Asp	Glu Glu	Glu Glu	Glu Glu	Glu Asp	Ser Gln	Ala	
	90		95		100			
gaa gtc ctg	aag gtc	atc agg	cag tct	gct ggg	caa aag	aca acc	tgt	508
Glu Val Leu	Lys Val	Ile Arg	Gln Ser	Ala Gly	Gln Lys	Thr Thr	Cys	
	105		110		115			
ggc cag ggt	ctg gaa	ggg ccc	tgg gag	cgc cca	ccc cct	ctg gat	gag	556
Gly Gln Gly	Leu Glu	Gly Pro	Trp Glu	Arg Pro	Pro Pro	Leu Asp	Glu	
	120		125		130		135	
tcc gag aga	gat gga	ggc tct	gag gac	caa gtg	gaa gac	cca gca	cta	604
Ser Glu Arg	Asp Gly	Gly Ser	Glu Asp	Gln Val	Glu Asp	Pro Ala	Leu	
	140		145		150			
agt gag cct	ggg gag	gaa cct	cag cgc	cct tcc	ccc tct	gag cct	ggc	652
Ser Glu Pro	Gly Glu	Glu Pro	Gln Arg	Pro Ser	Pro Ser	Glu Pro	Gly	
	155		160		165			
aca taggcacca	gcttgcattct	cccaggagga	agtggagggg	acatcgctgt				705
Thr								
tccccagaaa	cccactctat	cctcaccctg	ttttgtgctc	ttccccctgc	ctgctagggc			765
tgcggtttct	gacttctaga	agactaaggc	tggtctgtgt	ttgcttggtt	gcccaccttt			825
ggctgatacc	cagagaacct	gggcacttgc	tgcttgatgc	ccaccctgc	cagtcattcc			885
tccattcacc	cagcgggagg	tgggatgtga	gacagcccac	attggaaaat	ccagaaaacc			945
gggaacaggg	atttgccctt	cacaattcta	ctccccagat	cctctcccc	ggacacagga			1005
gaccacagg	gcaggacct	aagatctggg	gaaaggaggt	cctgagaacc	ttgaggtacc			1065
cttagatcct	tttctaccca	ctttcctatg	gaggattcca	agtcaccact	tctctcaccg			1125
gcttctacca	gggtccagga	ctaaggcgtt	tttctccata	gcctcaacat	tttggaatc			1185
ttcccttaat	cacccttgct	cctcctgggt	gcctggaaga	tggaactggca	gagacctctt			1245
tggttgcttt	tgtgctttga	tgccaggaat	gccgcctagt	ttatgtcccc	ggtggggcac			1305
acagcggggg	gcgccaggtt	ttccttgctc	cccagctgct	ctgccccctt	ccccttcttc			1365
cctgactcca	ggcctgaacc	cctcccgtgc	tgtaataaat	ctttgtaaag	aaaaaaaaaa			1425
aaaaaa								1431

<210> 90  
 <211> 168  
 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
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 35 40 45  
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln  
 50 55 60  
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr  
 65 70 75 80  
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu  
 85 90 95  
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser  
 100 105 110  
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu  
 115 120 125  
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp  
 130 135 140  
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg  
 145 150 155 160  
 Pro Ser Pro Ser Glu Pro Gly Thr  
 165

<210> 91  
 <211> 1417  
 <212> DNA  
 <213> Homo sapiens

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 <222> 48..1301

<220>  
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 <222> 1302..1417

<220>  
 <221> polyA\_signal  
 <222> 1360..1365

<220>  
 <221> polyA\_site  
 <222> 1402..1417

<400> 91  
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 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val  
 -20 -15 -10 -5  
 cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca 152  
 Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr  
 1 5 10  
 gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc 200  
 Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr  
 15 20 25  
 ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac 248  
 Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His  
 30 35 40  
 cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca 296  
 Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr  
 45 50 55 60  
 gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa 344  
 Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu  
 65 70 75  
 atc ctg gag agc ctg aat ttc aac ctc acg gag att ccg gag gct cag 392  
 Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln  
 80 85 90  
 atc cat gaa ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac 440  
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp  
 95 100 105  
 agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc 488  
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly  
 110 115 120  
 ctg aag cta gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac 536  
 Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His  
 125 130 135 140  
 tca gaa gcc ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa 584  
 Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys  
 145 150 155  
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<222> 734..1115

<220>

<221> polyA\_signal

<222> 1072..1077

<220>

<221> polyA\_site

<222> 1101..1115

<400> 93

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tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
ggaaaaacaa aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295
                               Met His Phe Gly Leu Leu
                               -15
tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
                               -10                               -5                               1
gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391
Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu
5                               10                               15                               20
aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439
Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
                               25                               30                               35
aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487
Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys
                               40                               45                               50
gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535
Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu
55                               60                               65
agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583
Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg
70                               75                               80
att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631
Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu
85                               90                               95                               100
gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679
Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr
                               105                               110                               115
aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727
Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp
120                               125                               130
gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggt 783
Ala Ile
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tggaagaatg cggtcatat ttaccaagtc tttctgaacg ccttctgcat tcatgcatcc 963
atgttctttc taggattgga tagcatttca tgccatgtgt aatatttggt cttttggcat 1023
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<211> 152

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..19







<210> 97  
 <211> 1855  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..117

<220>  
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 <222> 118..504

<220>  
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 <222> 505..1855

<220>  
 <221> polyA\_signal  
 <222> 1819..1824

<220>  
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 <222> 1840..1855

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 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165  
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu  
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 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro  
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 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala  
 10 15 20 25  
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309  
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu  
 30 35 40  
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357  
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe  
 45 50 55  
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405  
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
 60 65 70  
 atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu  
 75 80 85  
 tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501  
 Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val  
 90 95 100 105  
 gcc tgagccccac ttccccctca catgtgtctg ggcaccctgc aaggaccctg 554  
 Ala  
 cctcccaggc ccctggggca gccctccgc cgcagggttc aggtcccagg cccagctga 614  
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 cctgcccggc acccccggac cccctggccc cgcgggctcc ccggaaggca gcgccgcctg 854  
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 ggacgcgcgg cacaagcggg gacgcggaga catccgcgcg ttggtgcaac tgcacaacaa 974

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cgaggcgggc aggctggccg tgcggagcca caccgcgacc gagtgcaaat gccacgggct 1034
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cctccctccc cttggcctct aggaggaaac agtttttttag actggaaaaa agccagtcta 1754
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tatcaataaa gatatttaaa ccaccaaaaa aaaaaaaaaa a 1855

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 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro  
                     -5                    1                    5  
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala  
           10                    15                    20  
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu  
   25                    30                    35                    40  
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe  
                     45                    50                    55  
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
                     60                    65                    70  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu  
           75                    80                    85  
 Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val  
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 <212> DNA  
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Met Ile Val Lys Gly Val Ala  
1 5  
tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163  
Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser  
10 15 20  
tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211  
Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val  
25 30 35  
gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259  
Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile  
40 45 50 55  
ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307  
Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys  
60 65 70  
acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355  
Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile  
75 80 85  
aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403  
Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr  
90 95 100  
gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451  
Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu  
105 110 115  
tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499  
Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met  
120 125 130 135  
gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547  
Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val  
140 145 150  
gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595  
Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys  
155 160 165  
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Gln Thr Thr Val Lys Asn  
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Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn  
35 40 45  
Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val  
50 55 60  
Pro Val Lys Glu Leu Leu Lys Thr Ile Pro Lys Tyr Lys Leu Gly Ile  
65 70 75 80



Arg	Leu	Phe	Ser	Asp	Ala	Arg	Arg	Leu	Leu	Leu	Tyr	Ser	Gln	Lys	Asp	
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acc	agc	atg	aag	gac	atg	cg	aaa	gtt	ctg	aga	aca	tta	cag	cag	atc	558
Thr	Ser	Met	Lys	Asp	Met	Arg	Lys	Val	Leu	Arg	Thr	Leu	Gln	Gln	Ile	
120					125					130					135	
aag	aaa	tcc	agc	tca	aga	ggg	gac	aaa	cg	cat	ttc	ctc	aac	tgg	cag	606
Lys	Lys	Ser	Ser	Ser	Arg	Gly	Asp	Lys	Arg	His	Phe	Leu	Asn	Trp	Gln	
				140					145					150		
aag	gga	ctg	aag	cct	ctc	cct	caa	gcc	ctt	tta	taggggtcct	cattgtcagg				659
Lys	Gly	Leu	Lys	Pro	Leu	Pro	Gln	Ala	Leu	Leu						
				155					160							
cctctaagcc	caagccaagc	catcgcatcc	cctgtgactt	gcacatatat	gcccagatgg											719
cctgaagtaa	ctgaagaatc	acaaaagaag	tgaaaaggcc	ctgcctcgcc	ttactgatg											779
acgttccacc	attgtgattt	gttcctgccc	caccttaact	gagtgtatt	ccctgtgaat											839
ttccttctcc	tggtctagaa	gctccccac	tgagcacctt	gtgacccct	gcccctgccc											899
accagagaac	aacccccctt	gactgtaatt	ttccattacc	ttcccaaata	ctataaaaacg											959
gccccacccc	tatctccctt	tgctgactct	cttttcggac	tcagcccacc	tgcagccagg											1019
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 <213> Homo sapiens

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Phe	Arg	Arg	Arg	Gln	Thr	Cys	Gln	Leu	Leu	Leu	Glu	Val	Ala	Trp	Pro	
			20					25					30			
Leu	Phe	Ile	Phe	Leu	Ile	Leu	Ile	Ser	Val	Arg	Leu	Ser	Tyr	Pro	Pro	
		35				40					45					
Tyr	Glu	Gln	His	Glu	Cys	His	Phe	Pro	Asn	Lys	Ala	Met	Pro	Ser	Ala	
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Gly	Thr	Leu	Pro	Trp	Val	Gln	Gly	Ile	Ile	Cys	Asn	Ala	Asn	Asn	Pro	
65				70					75					80		
Cys	Phe	Arg	Tyr	Pro	Thr	Pro	Gly	Glu	Ala	Pro	Gly	Val	Val	Gly	Asn	
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Phe	Asn	Lys	Ser	Ile	Val	Ala	Arg	Leu	Phe	Ser	Asp	Ala	Arg	Arg	Leu	
			100					105					110			
Leu	Leu	Tyr	Ser	Gln	Lys	Asp	Thr	Ser	Met	Lys	Asp	Met	Arg	Lys	Val	
		115					120					125				
Leu	Arg	Thr	Leu	Gln	Gln	Ile	Lys	Lys	Ser	Ser	Ser	Arg	Gly	Asp	Lys	
	130					135					140					
Arg	His	Phe	Leu	Asn	Trp	Gln	Lys	Gly	Leu	Lys	Pro	Leu	Pro	Gln	Ala	
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 <222> 1172..1187

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ttg ttc tcg agt ttt ctc tgc cat gtt gct att gca gga cgg acc tgt	103
Leu Phe Ser Ser Phe Leu Cys His Val Ala Ile Ala Gly Arg Thr Cys	
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ccc aag cca gat gat tta cca ttt tcc aca gtg gtc ccg tta aaa aca	151
Pro Lys Pro Asp Asp Leu Pro Phe Ser Thr Val Val Pro Leu Lys Thr	
10 15 20	
ttc tat gag cca gga gaa gag att acg tat tcc tgc aag ccg ggc tat	199
Phe Tyr Glu Pro Gly Glu Glu Ile Thr Tyr Ser Cys Lys Pro Gly Tyr	
25 30 35	
gtg tcc cga gga ggg atg aga aag ttt atc tgc cct ctc aca gga ctg	247
Val Ser Arg Gly Gly Met Arg Lys Phe Ile Cys Pro Leu Thr Gly Leu	
40 45 50	
tgg ctc atc aac act ctg aaa tgt aca ccc aga gta tgt cct ttt gct	295
Trp Leu Ile Asn Thr Leu Lys Cys Thr Pro Arg Val Cys Pro Phe Ala	
55 60 65	
gga atc tta gaa aat gga gcc gta cgc tat acg act ttt gaa tat ccc	343
Gly Ile Leu Glu Asn Gly Ala Val Arg Tyr Thr Thr Phe Glu Tyr Pro	
70 75 80 85	
aac acg atc agt ttt tct tgt aac act ggg ttt tat ctg aat ggc gct	391
Asn Thr Ile Ser Phe Ser Cys Asn Thr Gly Phe Tyr Leu Asn Gly Ala	
90 95 100	
gat tct gcc aag tgc act gag gaa gga aaa tgg agc ccg gag ctt cct	439
Asp Ser Ala Lys Cys Thr Glu Glu Gly Lys Trp Ser Pro Glu Leu Pro	
105 110 115	
gtc tgt gct ccc atc atc tgc cct cca cca tcc ata cct acg ttt gca	487
Val Cys Ala Pro Ile Ile Cys Pro Pro Pro Ser Ile Pro Thr Phe Ala	
120 125 130	
aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg	535
Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg	
135 140 145	
gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat	583
Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn	
150 155 160 165	
gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa	631
Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu	
170 175 180	
tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt	679
Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe	
185 190 195	
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Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr	
200 205 210	
ttt ggc tgc cat gat gga tat tct ctg gat ggc ccg gaa gaa ata gaa	775



Phe Gly Cys His Asp Gly Tyr Ser Leu Asp Gly Pro Glu Glu Ile Glu  
 215 220 225  
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 Cys Thr Lys Leu Gly Asn Trp Ser Ala Met Pro Ser Cys Lys Ala Ser  
 230 235 240 245  
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 Cys Lys Val Pro Val Lys Lys Ala Thr Val Val Tyr Gln Gly Glu Arg  
 250 255 260  
 gta aag att cag gaa aaa ttt aag aat gga atg cta cat ggt gat aaa 919  
 Val Lys Ile Gln Glu Lys Phe Lys Asn Gly Met Leu His Gly Asp Lys  
 265 270 275  
 gtt tct ttc ttc tgc aaa aat aag gaa aag aag tgt agc tat aca gag 967  
 Val Ser Phe Phe Cys Lys Asn Lys Glu Lys Lys Cys Ser Tyr Thr Glu  
 280 285 290  
 gat gct cag tgt ata gat ggc act atc gaa gtc ccc aaa tgc ttc aag 1015  
 Asp Ala Gln Cys Ile Asp Gly Thr Ile Glu Val Pro Lys Cys Phe Lys  
 295 300 305  
 gaa cac agt tct ctg gct ttt tgg aaa act gat gca tcc gat gta aag 1063  
 Glu His Ser Ser Leu Ala Phe Trp Lys Thr Asp Ala Ser Asp Val Lys  
 310 315 320 325  
 cca tgc taaggtggtt ttcagattcc acataaaatg tcacacttgt ttcttgttca 1119  
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 aaaaaaaaa 1187

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 <212> PRT  
 <213> Homo sapiens

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 30 35 40 45  
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 Pro Arg Val Cys Pro Phe Ala Gly Ile Leu Glu Asn Gly Ala Val Arg  
 65 70 75  
 Tyr Thr Thr Phe Glu Tyr Pro Asn Thr Ile Ser Phe Ser Cys Asn Thr  
 80 85 90  
 Gly Phe Tyr Leu Asn Gly Ala Asp Ser Ala Lys Cys Thr Glu Glu Gly  
 95 100 105  
 Lys Trp Ser Pro Glu Leu Pro Val Cys Ala Pro Ile Ile Cys Pro Pro  
 110 115 120 125  
 Pro Ser Ile Pro Thr Phe Ala Thr Leu Arg Val Tyr Lys Pro Ser Ala  
 130 135 140  
 Gly Asn Asn Ser Leu Tyr Arg Asp Thr Ala Val Phe Glu Cys Leu Pro  
 145 150 155  
 Gln His Ala Met Phe Gly Asn Asp Thr Ile Thr Cys Thr Thr His Gly  
 160 165 170  
 Asn Trp Thr Lys Leu Pro Glu Cys Arg Glu Val Lys Cys Pro Phe Pro  
 175 180 185  
 Ser Arg Pro Asp Asn Gly Phe Val Asn Tyr Pro Ala Lys Pro Thr Leu  
 190 195 200 205







Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu  
 370 375 380  
 Leu Ala Arg Arg Gln Arg Arg Arg Gln Ala Arg Arg Glu Ala Glu Ala  
 385 390 395 400  
 Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile  
 405 410 415  
 Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys  
 420 425 430  
 Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg  
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 Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys  
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<220>  
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 <222> 95..1252

<220>  
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 tctgccaagc ttctccgata cccaggtttc ataa atg tgt ttg ttg ctt tcc tgc 115  
 Met Cys Leu Leu Leu Ser Cys  
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 cct tgc cac ccc tct gcc cac gga cag tcc atg tgg att gag aga acc 163  
 Pro Cys His Pro Ser Ala His Gly Gln Ser Met Trp Ile Glu Arg Thr  
 -5 1 5  
 tcc ttc gtg act gca tac aag ctg ccg ggg atc ctg cgc tgg ttt gag 211  
 Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp Phe Glu  
 10 15 20 25  
 gtg gtg cac atg tcg cag acc aca att agt cct ctg gag aat gcc ata 259  
 Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn Ala Ile  
 30 35 40  
 gaa acc atg tcc acg gcc aat gag aag atc ctg atg atg ata aac cag 307  
 Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu Met Met Ile Asn Gln  
 45 50 55  
 tac cag agt gat gag acc ctc ccc atc aac cca ctc tcc atg ctc ctg 355  
 Tyr Gln Ser Asp Glu Thr Leu Pro Ile Asn Pro Leu Ser Met Leu Leu  
 60 65 70  
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 75 80 85



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 <211> 386  
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 <213> Homo sapiens

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 <222> 1..15

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 Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys  
 35 40 45  
 Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile  
 50 55 60 65  
 Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met  
 70 75 80  
 Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val  
 85 90 95  
 Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu  
 100 105 110  
 Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu  
 115 120 125  
 Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu  
 130 135 140 145  
 Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg  
 150 155 160  
 Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met  
 165 170 175  
 Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn  
 180 185 190  
 Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu  
 195 200 205  
 Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile  
 210 215 220 225  
 Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys  
 230 235 240  
 Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala  
 245 250 255  
 Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp  
 260 265 270  
 Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu  
 275 280 285  
 Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu  
 290 295 300 305  
 Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser  
 310 315 320  
 Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys  
 325 330 335  
 Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala  
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 Ser Lys Ser Ala Glu Glu Gly Lys Gln Ile Pro Asp Ser Leu Ser Thr  
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<210> 111

<211> 1408  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..102

<220>  
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<220>  
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 <222> 1264..1408

<220>  
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<220>  
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 Met Ser Thr Phe  
 1  
 ttc tcg gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt 162  
 Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys  
 5 10 15 20  
 ggg aca gta ttt tgc aaa tac aag aag agc tca ggg cag ctg tgg agc 210  
 Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly Gln Leu Trp Ser  
 25 30 35  
 tgg atg gtc tgc ctg gca ggc ctc tgt gca gtc tgc ctg ctc atc ctg 258  
 Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Leu Ile Leu  
 40 45 50  
 tcc cct ttt tgg ggc ttg atc ctc ttc tcg gtg tca tgc ttc ctc atg 306  
 Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met  
 55 60 65  
 tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca 354  
 Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala  
 70 75 80  
 gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag 402  
 Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys  
 85 90 95 100  
 tat ctg gat gag ctg ggc ttc acg gta ttt gcc gga gtt ttg aat gaa 450  
 Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly Val Leu Asn Glu  
 105 110 115  
 aat ggc cca gga gct gag gaa ttg cga aga acc tgc tct ccg cgc ctc 498  
 Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys Ser Pro Arg Leu  
 120 125 130  
 tcg gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct 546  
 Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala  
 135 140 145  
 tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg 594  
 Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val  
 150 155 160  
 atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt 642  
 Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu  
 165 170 175 180  
 ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act 690





FOUO "SECRET"

	115					120						125					
Ser	Pro	Arg	Leu	Ser	Val	Leu	Gln	Met	Asp	Ile	Thr	Lys	Pro	Val	Gln		
	130					135						140					
Ile	Lys	Asp	Ala	Tyr	Ser	Lys	Val	Ala	Ala	Met	Leu	Gln	Asp	Arg	Gly		
145					150					155					160		
Leu	Trp	Ala	Val	Ile	Asn	Asn	Ala	Gly	Val	Leu	Gly	Phe	Pro	Thr	Asp		
				165					170					175			
Gly	Glu	Leu	Leu	Leu	Met	Thr	Asp	Tyr	Lys	Gln	Cys	Met	Ala	Val	Asn		
			180					185					190				
Phe	Phe	Gly	Thr	Val	Glu	Val	Thr	Lys	Thr	Phe	Leu	Pro	Leu	Leu	Arg		
	195						200					205					
Lys	Ser	Lys	Gly	Arg	Leu	Val	Asn	Val	Ser	Ser	Met	Gly	Gly	Gly	Ala		
210					215						220						
Pro	Val	Glu	Arg	Leu	Ala	Ser	Tyr	Gly	Ser	Ser	Lys	Ala	Ala	Val	Thr		
225					230						235				240		
Met	Phe	Ser	Ser	Val	Met	Arg	Leu	Glu	Leu	Ser	Lys	Trp	Gly	Ile	Lys		
				245					250					255			
Val	Ala	Ser	Ile	Gln	Pro	Gly	Gly	Phe	Leu	Thr	Asn	Ile	Ala	Gly	Thr		
			260					265				270					
Ser	Asp	Lys	Trp	Glu	Lys	Leu	Glu	Lys	Asp	Ile	Leu	Asp	His	Leu	Pro		
	275						280					285					
Ala	Glu	Val	Gln	Glu	Asp	Tyr	Cys	Gln	Asp	Tyr	Ile	Leu	Ala	Gln	Arg		
290					295						300						
Asn	Phe	Leu	Leu	Leu	Ile	Asn	Ser	Leu	Ala	Ser	Lys	Asp	Phe	Ser	Pro		
305					310					315					320		
Val	Leu	Arg	Asp	Ile	Gln	His	Ala	Ile	Leu	Ala	Lys	Ser	Pro	Phe	Ala		
				325					330					335			
Tyr	Tyr	Thr	Pro	Gly	Lys	Gly	Ala	Tyr	Leu	Trp	Ile	Cys	Leu	Ala	His		
			340					345					350				
Tyr	Leu	Pro	Ile	Gly	Ile	Tyr	Asp	Tyr	Phe	Ala	Lys	Arg	His	Phe	Gly		
	355						360					365					
Gln	Asp	Lys	Pro	Met	Pro	Arg	Ala	Leu	Arg	Met	Pro	Asn	Tyr	Lys	Lys		
	370					375					380						
Lys	Ala	Pro															
385																	